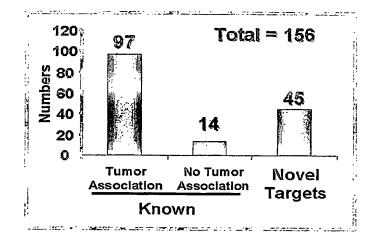


5 Figure 1. Advantage of Efficacy-First Discovery™ Method



10 Figure 2. Highly Enriched Tumor Targets

siRNA-Mediated Target Validation (MDA-MB-435 Xenograft Model) 1400 P<0.01, N = 81200 Tumor Size (mm³) ← ICTE1030-siRNA (Cell Surface Protein) -D--ICTB1031-siRNA (Ligand) - GFP-siRNA 800 P<0.05 400 10 24 27 **Days After Tumor Cell Inoculation**

Figure 3. Two Novel Targets Were Validated

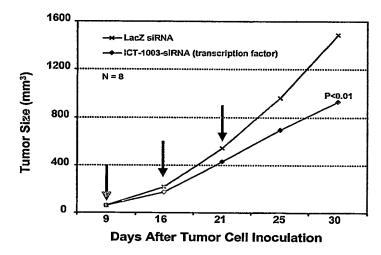


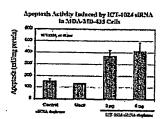
Figure 4. A Novel Targets Was Validated

5

ICT1024, a growth factor receptor like protein

In vivo In vitro

Apoptosis Activity



ICT-1024 siRNA mediated tumor growth inhibition in MDA-MB-435/nude mice model

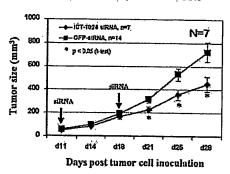
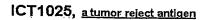


Figure 5.



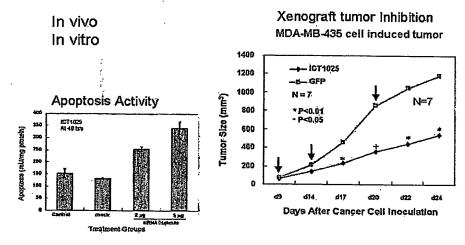
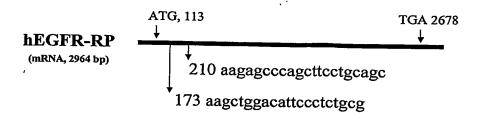


Figure 6.

5

Figure 7

ICT-1024 siRNA Design:



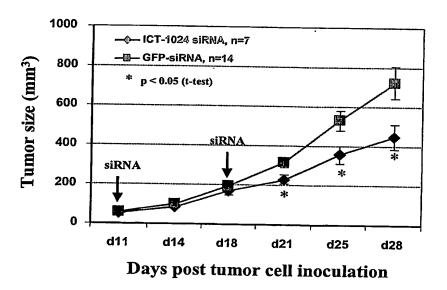


Figure 9. **Apoptosis Activity Induced by ICT-1024 siRNA**in MDA-MB-435 Cells

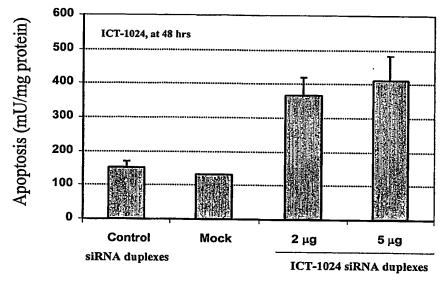


Figure 10. SAGE/Microarray Data

CGAP SAGE
Expression Data
and Correlation:
ICT1024 has
significantly
positive correlation
with other breast
cancer genes

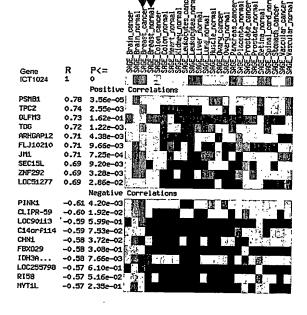
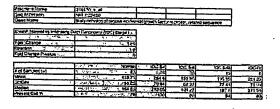
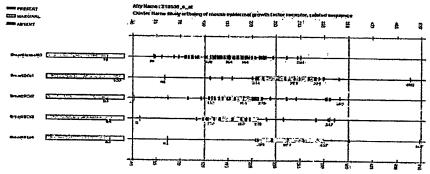


Figure 11 Cancer Tissue Distribution





ICT1024 is highly up regulated in all Stage I Breast Tumor samples (100%)

Figure 12. Consensus in rhomboid family

			10	20	30	40	50	60	
			• • • • • • • •	* .] •	• •] •	· · · · · · · · • · · · ·	1
Human	consensus	1	PLQPGQL	WRLITS	MPLHAGILHI	LENMLSLLFF	GIPLERRLGS	VRFLLLYLLSGLAG	- 57
Yeast	gi 9963865	99	ALRNWQV:	YRLVTY	i Pvyenp isi	LCGAIIIWRF	AGNFERTVGT	TVRHCFFTVIFAIFS	- 155
Bacteria	gi 3738201	47	LLQKRQL	YBIITY\	VTLHLSMLHI	VFNFVSLLPA	MSOFEKKOGT	LACILVIVIPYTLE	n 104
Yeast	gi 1653749	49	PRSLEGL	RGIVFAI	PFLHADFGHI	LIANSVPFVVL	AWLVMLO-EV	SDFWIVTIITMVVG	- 104
Human	gi 13621505	60	akanarpy	vva igdsD1	LYSYRIWS-E	FCQWINTIFC	WSNRRRPLGI	TPFLLLYVLSGVMG	- 117
Bacteria	gi 20139804	103	PEICREEAU	rFisy	ILVHAGVQH1	LGNLCMOLVL	GIPLEMVHKO	LRVGLVYLAGVIAG	- 159
Human	gi 1169951	129	PTLKPEF	RYFTH	ALMHPSLMHI	LENLLWWWYL	GGAVEKRLGS	GKLIVIRSISALLS	- 185
	gi 11066250	198	SNPASKVI	LCspMLLS1	Cesheslehn	IAANMYVLNSF:	SSSIVNILGO	EQFMAVYLSAGVIS	- 256
Bacteria	gi 13813618	68	yLVI KGYN	Se-LFTS	FITNSFVDE	I FNFISLYVI	YLIFGSRAGE	CHEYGIFILAGILGN	- 125
Plant	gi 9294149	242	IPKHKOL	CRLFLSA	YEAR THE SHE	VYNMISLLWK	GIKLETSMGS	Sepasmyptligms	- 298
				70	80	90	100	110 1	20
			*	* .] *	·] *] •	·	Ī
Human	consensus	58	SLLSLLLS	PAS	-TPSVGASGA	I FGLLGALLV	LLPLNRILLL	NPGAALFLLIGI	I 110
Yeast	g1 9963865	156	aiiflspe	:82VA	LSKLGBVED	argptpvapai	MLGVTTVRSR	MRraLVFGMVVPSV	L 211
Bacteria	gi 3738201	105	GIMHLIV	(HFF1 rkd)	/VS IAGLSGW	IAFAFISASCV	HSPQRLISFF	NLFSIPAYC	P 159
Yeast	gi 1653749	105	GLGVWLI#	/PPN	TVTVGASIL	I FGYLGPLLF	RGWFQKNLAS	IV1-SIVVLVLYGS	A 158
Human	gi 13621505	118	NAFTFWLI	PETv	AAGASTS	LFGLPAAIVV	LSFLGKNQAL	KDI-GKSYQTLIV-	V 169
Bacteria	gi 20139804	160	SLASSIFE)PLR	-YLVGASGG	VYALMGGYFM	NVLVNFQEMI	PAFGIPRLLIII	L 211
Human	gi 1169951	186	GYVQQKPS	GPW	FGGLSGV	VYALMGYVWLI	RGERDPOSG-	IYLORGL	I 230
Bacteria	gi 11066250	257	nfvsylgh	WATgry	/GPSLGASGA	IMTVLAAVCT	KIPEGR-LA-	IIFLPMFT	F 306
	gl 13813618	126	LLTVIPYS	PFT	-LSSGASGG	I FGLLSYYTP:	YDFLKKONLG	VYGLVFLVSV	2 175
Plant	gi 9294149	299	QGVTLLLA	KSL	LLLFDYDRA	YYNEYAVGFS	3VLFAMKVVL	NSq-AEDYSSVYGI	L 352
				130	140	150	160	170	
Human			*****] • .	•].	
Yeast	consensus	111	LLNLLLGL	LPGIS	NFG	HLGG1	Llagilligpi	LLRRPR 146	
	gi 9963865	212	VPWLLLGA	swlipQTS	FLS	NVCGI	LSIGLAYAHL	LLPHRP 250	
Bacteria	gi 3738201	160	PIIYLIMT	'tilvpkas	FIG	HASG	AVMGYCTPFM	LGSIPL 198	
Yeast	gi 1653749	159	LWGLLPGR	AGVS	WQG	HLFG	Pigga Laawl	IAREKH 193	
Human	gi 13621505	170	NLLMNLP-	MPNVS	MAG	HIGG\	/VGGALLS I V	FPTKMR 204	
Bacteria	gi 20139804	212	IIVLDMGF	Alyrr	FFVpedgsp	-vsfaaHIAGC	FAGMSIGYT	VFSCFD 258	
Human	gi 1169951	231	IFALIWIV	AGWFD	LFGmsma	ngaHIAGI	Lavglamaev	DSLNAR 273	
Bacteria	gi 11066250	307	TAGNALKA	IIAMD	TAGmilgwk	f fdhaaHLGG/	LFGI WYVTY	GHELIW 354	
Plant	gi 13813618	176	GVSDLIPP	NVN	VVA	HIGG1	LGGIMYAVV	YYLIRS 209	
	gi 9294149	353	VPTKYAAW	a-eLILVQ	MFVpnas	flgHLGGI	LAGI IYLKL	KGSYSG 397	

Figure 13.

Human rhomboid Proteins

Human Rhomboid Family Protein Alignments

17CT-1024 HRhomboid 2 HRhomboid 3 HRhomboid 4 HRhomboid 4 HRhomboid 6 HRhomboid 6 HRhomboid 6 HRhomboid 7 HRhomboid 6 105 105 HRhomboid 6 105 105 HRhomboid 6 105 105 HRhomboid 6 105	mecarrdotselqrkypwikldypavpicae-epsflqplrrqsflsevsmpaerahissphhalrrpvlqrqtsitqrirrgtadwfgvskdodsrdwqrkairhcoqry mecasgings mecasging	rrar-ristpasfleedtdfpdeldioffaregilheelstypdevfeopscaalidvekapeqoditggaldreelstellijjargwikdpegaaapqpkvilrqevveta qrcrvvkrsfatpefleedtdfooffaregilheelstypdevfeopscaalidvekapeqoditggaldreelstellijjargwikdpegaaapqpkvilrqevveta qrcrvvkrsfatpefleedtdooffaseffskeensempdovfeopplaa-syfrajphsagegdkrakkhukvygrappy	gprzgqrapyralGarekryyglawgrlinztyrkridafvkrqiedmddhzpfftywlifyhalvtilavciygiap-wgfaqhetwdavinnzgypanykyqqentwigsae 11wakwalphetworg yavgaminzyrzaisarvqqqaafdahydliliyaryalawhinayrzaisarvqqqaafdahydliliyaryalawhinayrzaisarvqqqaafdahydliliyaryalawhinayrzaisarvqqqaafdahydliliyaryalawhinayrzaisarvqqqaaafdahydliliyaryalawhinayrzaisarvqqqaaaqdahydliliyaryalawhinayraafaayaaanyyaanykyaanyyaanyyaanyyaanyyaa	### ### ##############################	vtgnlasaı[1pyraovypagaqgılaclfvelfga-vqılarpxraff-kllavvlfifttgl-lpw-j	pyisfyktdlyrkrogilifovklyllaglvylkyvyroroewceiltcipitchyeldaglh
	11 12 14 17 18 18 18 18 18 18 18 18 18 18 18 18 18	234 13 26 108 71 97		213 213 213 204 348 348 204 196 243	101 157 465 259 259 254 287	253 7 252 3 352 3 345 3
		ICT-1024 HRhomboid 3 HRhomboid 3 HRhomboid 4 HRhomboid 5		HRhomboid 4 HRhomboid 5 HRhomboid 6 ICT-1024 HRhomboid 2 HRhomboid 4 HRhomboid 4 HRhomboid 6 HRhomboid 6		

Figure 14. Function Domain Homology

ICT-1024, A Novel Member of Rhomboid Family

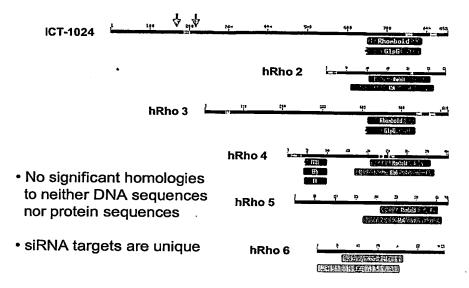
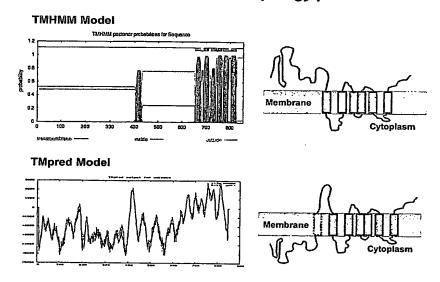


Figure 15. Hydrophobicity Analysis

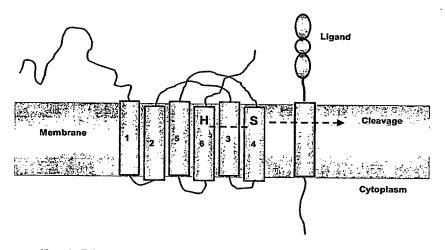
Cellular Location and Topology predictions



Activation of EGFRs and ligands

Figure 16.

ICT-1024 Intramembrane Protease Activity



Refer to Koonin EV, et al. Genome Biology, 2003

Figure 17.

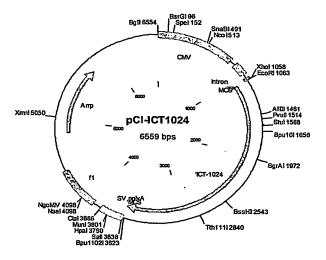


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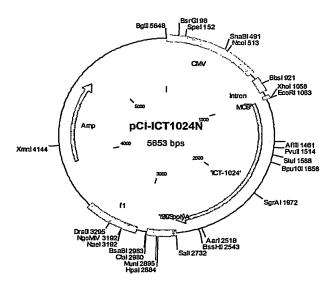


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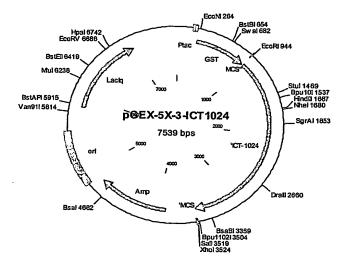


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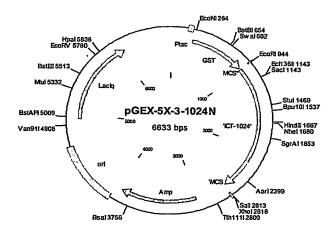


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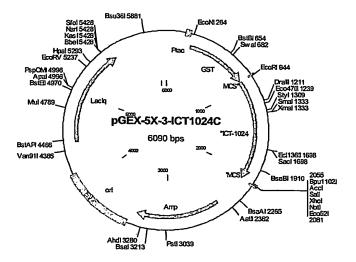


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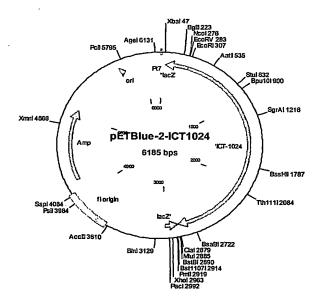


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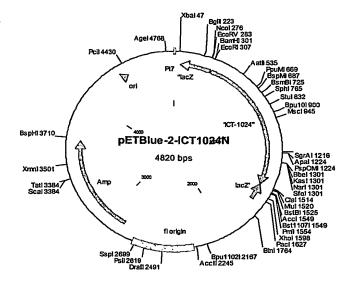


Figure 24

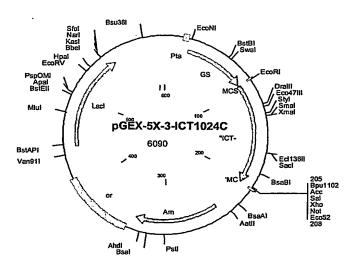


Fig. 25 (SEQ ID NO:58) ICT1024 PROTEIN (855 AA) CODING REGION: 1670-3637

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121	AATATGACCG	CCATGTTGGC	ATTGATTATT	ATTGATTATT GACTAGTTAT TAATAGTAAT CAATTACGGG	TAATAGTAAT	CAATTACGGG
181	GTCALTAGIT	GTCATTAGTT CATAGCCCAT	ATATGGAGTT	CCGCGTTACA	CCGCGTTACA TAACTTACGG	TAAATGGCCC
241	GCCTGGCTGA	CCGCCCAACG	CCGCCCAACG ACCCCCCGCCC	ATTGACGTCA	ATAATGACGT	ATGTTCCCAT
301	AGTAACGCCA	AGTAACGCCA ATAGGGACTT	TCCATTGACG		TCAATGGGTG GAGTATTTAC GGTAAACTGC	GGTAAACTGC
361	CCACTTGGCA	CCACTTGGCA GTACATCAAG TGTATCATAT GCCAAGICCG CCCCCTAITG ACGICAAIGA	TGTATCATAT	GCCAAGTCCG	CCCCCTATIG	ACGTCAATGA
421	CGGTAAATGG	CGGTAAATGG CCCGCCTGGC	ATTATGCCCA	ATTATGCCCA GTACATGACC TTACGGGACT	TTACGGGACT	TTCCTACTTG
481	GCAGTACATC	TACGTATTAG	TCATCGCTAT	TACCATGGTG ATGCGGTTTT	ATGCGGTTTT	GGCAGTACAC
541	CAATGGGCGT	GGATAGCGGT	TTGACTCACG	GGGATTTCCA AGTCTCCACC	AGTCTCCACC	CCATTGACGT
601	CAATGGGAGT	CAATGGGAGT ITGITITGGC ACCAAAATCA ACGGGACTIT CCAAAAIGIC GIAATAACCC	ACCAAAATCA	ACGGGACTTT	CCAAAATGTC	GTAATAACCC
199	ರದ್ದರುವಾರು	ACGCAAATGG	GCGGTAGGCG	GCGGTAGGCG TGTACGGTGG	GAGGTCTATA	TAAGCAGAGC
721	TCGTTTAGTG	AACCGTCAGA	TCACTAGAAG	CTTTATTGCG GTAGITTAIC		ACAGTTAAAT
781	TGCTAACGCA	TGCTAACGCA GTCAGTGCTT	CTGACACAAC	CTGACACAAC AGTCTCGAAC TTAAGCTGCA GAAGTTGGTC	TTAAGCTGCA	GAAGTTGGTC
841	GTGAGGCACT	GTGAGGCACT GGGCAGGTAA GTATCAAGGT TACAAGACAG GTTTAAGGAG ACCAATAGAA	GTATCAAGGT	TACAAGACAG	GTTTAAGGAG	ACCAATAGAA
901	ACTGGGCTTG	TCGAGACAGA	GAAGACTCTT	TCGAGACAGA GAAGACTCTT GCGTTTCTGA	TAGGCACCTA	TTGGTCTTAC
961	TGACATCCAC	TTTGCCTTTC	TCTCCACAGG	TITGCCITIC ICTCCACAGG IGTCCACTCC CAGITCAAIT ACAGCICTIA	CAGTTCAATT	ACAGCTCTTA

AGGCTAGAGT ACTTAATACG ACTCACTATA GGCTAGCCTC GAGAATTCCA TGAGTGAGGC CCGCAGGGAC AGCACGAGCA GCCTGCAGCG CAAGAAGCCA CCCTGGCTAA AGCTGGACAT TCCCTCTGCG GTGCCCCTGA CGGCAGAAGA GCCCAGCTTC CTGCAGCCCC TGAGGCGACA GGCTTTCCTG AGGAGTGTGA GTATGCCAGC CGAGACAGCC CACATCTCTT CACCCCACCA TGAGCTCCGG CGGCCGGTGC TGCAACGCCA GACGTCCATC ACACAGACCA TCCGCAGGGG GACCGCCGAC TGGTTTGGAG TGAGCAAGGA CAGTGACAGC ACCCAGAAAT GGCAGCGCAA GAGCATCCGT CACTGCAGCC AGCGCTACGG GAAGCTGAAG CCCCAGGTCC TCCGGGAGCT GGACCIGCCC AGCCAGGACA ACGIGICGCI GACCAGCACC GAGACGCCAC CCCCACICIA CGIGGGGCCA IGCCAGCIGG GCAIGCAGAA GAICAIAGAC CCCCIGGCCC GIGGCCGIGC CTTCCGTGTG GCAGATGACA CTGCGGAAGG CCTGAGTGCC CCACACACTC CCGTCACGCC GGGTGCTGCC TCCCTCTGCT CCTTCTCCAG CTCCCGCTCA GGTTTCCACC GGCTCCCGCG GCGGCGCAAG CGAGAGTCGG TGGCCAAGAT GAGCTTCCGG GCGGCCGCAG CGCTGATGAA AGGCCGCTCC GTTAGGGAIG GCACCTTTCG CCGGGCACGG CGTCGAAGCT TCACTCCAGC TAGCITICIG GAGGAGGACA CAACIGAIIT CCCCGAIGAG CIGGACACAI CCIICTIIGC CCGGGAAGGT ATCCTCCATG AAGAGCTGTC CACATACCCG GATGAAGTTT TCGAGTCCCC ATCGGAGGCA GCGCTAAAGG ACTGGGAGAA GGCACCGGAG CAGGCGGACC TCACCGGCGG GGCCCTGGAC CGCAGCGAGC TTGAGCGCAG CCACCTGATG CTGCCCTTGG AGCGAGGCTG GCGGAAGCAG AAGGAGGGCG CCGCAGCCCC GCAGCCCAAG GTGCGGCTCC GACAGGAGGT GGTGAGCACC GCGGGCCGC GACGGGCCA GCGTATCGCG GTGCCGGTGC GCAAGCTCTT 1501 1021 1081 1141 1201 1321 1381 1261 1561 1621 1681 1801 1861 1921 1981 2041 2101

CGCCCGGGAG AAGCGGCCGT ATGGGCTGGG CATGGTGGGA CGGCTCACCA ACCGCACCTA CTATGGCATC GCGCCCGTGG GCTTCTCGCA GCATGAGACG GTGGACTCGG TGCTGCGGAA CCGCAAGCGC ATCGACAGCT TCGTCAAGCG CCAGATCGAG GACATGGACG ACCACAGGCC CTICITCACC TACTGGCTTA CCTTCGTGCA CTCGCTCGTC ACCATCCTAG CCGTGTGCAT CCGCGGGGTC TACGAGAACG TCAAGTACGT GCAGCAGGAG AACTTCTGGA TCGGGCCCAG GGTGCACAGC ITCATICGCT CGGCGCGCGA GCGCGAGAAG CACTCCGCCT GCTGCGIGCG CTCGGAGGCC CTCATCCACC TGGGCGCCAA GTTTTCGCCC TGCATGCGCC AGGACCCGCA CAACGACAGG TCGGGCTGCG TGCAGACCTC GGAGGAGGAG TGCTCGTCCA CGCTGGCAGT GIGGGIGAAG IGGCCCAICC AICCCAGCGC CCCAGAGCII GCGGGCCACA AGAGACAGII TGGCTCTGTC TGCCACCAGG ATCCCAGGGT GTGTGATGAG CCCTCCTCCG AAGACCCTCA TGAGTGGCCA GAAGACATCA CCAAGTGGCC GATCTGCACC AAAAACAGCG CTGGGAACCA CACCAACCAT CCCCACATGG ACTGTGTCAT CACAGGACGG CCCTGCTGCA TTGGCACCAA GGGCAGGTGT GAGATCACCT CCCGGGAGTA CTGTGACTTC ATGAGGGGCT ACTTCCATGA TCTCAACCCC GAGGIGCCIG ACCAGITCIA CCGCCIGIGG CIAICCCICI ICCIGCACGC GGAGGCCACG CICTGCICIC AGGIGCACIG CAIGGAIGAI GIGIGIGGGC ICCIGCCITI CGGGATCTIG CACTGCCTGG TGTCCATCTG CTTCCAGATG ACTGTCCTGC GGGACCTGGA GAAGCTGGCA GGCTGGCACC GCATAGCCAT CATCTACCTG CTGAGTGGTG TCACCGGCAA CCTGGCCAGT GCCATCTTCC TGCCATACCG AGCAGAGGTG GGTCCTGCTG GCTCCCAGTT CGGCATCCTG GCCTGCCTCT TCGTGGAGCT CTTCCAGAGC TGGCAGATCC TGGCGCGCGC 2161 2221 2281 2341 2401 2461 2521 2581 2641 2701 2761 2821 2881 2941 3001 3061 3121 3181 3241

CTGGCGTGCC TICTTCAAGC TGCTGGCTGT GGTGCTCTTC CTCTTCACCT TTGGGCTGCT GCTGCCAGAT TCCTCTCTT GCAGACATGA TAAGATACAT TGATGAGTTT GGACAAACCA CAACTAGAAT GCAGTGAAAA AAATGCTTTA TTTGTGAAAT TTGTGATGCT ATTGCTTTAT TTGTAACCAT TATAAGCTGC AATAAACAAG TTAACAACAA CAATTGCATT CATTTTATGT TTCAGGTTCA GGGGGAGATG AATGGCGAAT GGACGCGCC TGTAGCGGCG CATTAAGCGC GGCGGGTGTG GTGGTTACGC CATCATCITT CAGGIGGICT ICCIGGGCCT CCIGGCIGGC CIGGIGGICC ICTICIACGI CTGACAAGTT CTGTGAGAAG TACGAACTGG ACGCTCAGCT CCACTGAGTC GACCCGGGCG GCCGCTTCGA TITRAAGCAA GIAAAACCIC IACAAAIGIG GIAAAAICGA IAAGGAICCG GGCIGGCGIA AIAGCGAAGA GGCCCGCACC GAICGCCCII CCCAACAGII GCGCAGCCIG CCTTTCTCGC CACGTTCGCC GGCTTTCCCC GTCAAGCTCT AAATCGGGGG CTCCCTTTAG GCAGCGTGAC CGCTACACTT GCCAGCGCCC TAGCGCCCGC TCCTTCGCT TTCTTCCCTT GGTTCCGATT TAGAGCTTTA CGGCACCTCG ACCGCAAAAA ACTTGATTTG GGTGATGGTT CACGIAGIGG GCCAICGCCC IGAIAGACGG ITITICGCCC IIIGACGIIG GAGICCACGI TCTTTAATAG TGGACTCTTG TTCCAAACTG GAACAACACT CAACCCTATC TCGGTCTATT CTITIGATIT ATAAGGGAIT TIGCCGAITT CGGCCTAITG GITAAAAAI GAGCIGAITI AACAAATATT TAACGCGAAT TTTAACAAA TATTAACGTT TACAATTTCG CCTGATGCGG GCCGTGGATT GACAACTTTG CCCACATCTC GGGGTTCATC AGTGGCCTCT CGCCTTCTTG CCCTACATCA GCTTTGGCAA GTTCGACCTG TACCGGAAAC CTAICCIGIC CGCIGIGAGI GGIGIGAGII CCICACCIGC AICCCCIICA IGGGAGGTTT 3301 3361 3421 3481 3541 3601 3661 3721 3781 3841 3901 3961 4021 4081 4141 4201 4261 4321 438I

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4561	CCCTGACGGG	CTTGTCTGCT	CCCGGCATCC	GCTTACAGAC	AAGCTGTGAC	CGICICCGGG
4621	AGCTGCATGT	GTCAGAGGTT	TTCACCGTCA	TCACCGAAAC	GCGCGAGACG	AAAGGGCCTC
4681	GTGATACGCC	TATTTTATA	GGTTAATGTC	ATGATAATAA	TGGTTTCTTA	GACGTCAGGT
4741	GGCACTTTC	GĠGGAAATGT	GCGCGGAACC	CCTATTTGTT	TATTTTCTA	AATACATTCA
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5401	ACGATGCCTG	TAGCAATGGC	AACAACGTTG	CGCAAACTAT	TAACTGGCGA	ACTACTTACT
5461	CTAGCTTCCC	GGCAACAATT	AATAGACTGG	ATGGAGGCGG ATAAAGTTGC	ATAAAGTTGC	AGGACCACTT
5521	CTGCGCTCGG	CIGCGCICGG CCCTICCGGC	TGGCTGGTTT	ATTGCTGATA AATCTGGAGC		CGGTGAGCGT

				GACAGATCT	CACATGGCTC GACAGATCT	6541
GCCTTTTGCT	CCTTTTGCTG	CGGTTCCTGG	GGCCTTTTTA	CCAGCAACGC	TGGAAAAACG	6481
GCGGAGCCTA	CGTCAGGGGG	TTGTGATGCT	GCGTCGATTT	TITCGCCACC ICTGACTTGA GCGTCGAITT	TTTCGCCACC	6421
rccrercess	ATCTTTATAG	AACGCCTGGT	TCCAGGGGGA	CGAGGGAGCT	GGAGAGCGCA	6361
GGTCGGAACA	TAAGCGGCAG	AGGTATCCGG	AAAGGCGGAC	CCGAAGGGAG	GCCACGCTTC	6301
ATGAGAAAGC	AGCGTGAGCT	AGATACCTAC	CACCGAACTG	AGCTTGGAGC GAACGACCTA CACCGAACTG	AGCTTGGAGC	6241
CACACAGCCC	GGGGTTCGTG	GGCTGAACGG	GCAGCGGTCG	CGATAGTTAC CGGATAAGGC GCAGCGGTCG GGCTGAACGG GGGGTTCGTG	CGATAGTTAC	6181
GGACTCAAGA	TTACCGGGTT	AAGTCGTGTC	CAGTGGCGAT	TGGCTGCTGC	CTGTTACCAG	6121
: TCTGCTAATC	CATACCTCGC	GCACCGCCTA	ĠAACTCTGTA	ACCACTTCAA	TAGTTAGGCC	6061
AGTGTAGCCG	CIGICCIICI	ATACCAAATA	CAGAGCGCAG	CTGGCTTCAG	CCGAAGGTAA	6001
AAGAGCTACC AACTCTTTT	AAGAGCTACC	TIGCCGGAIC	GGTGGTTTGT	AAAAAACCAC CGCTACCAGC GGTGGTTTGT TTGCCGGATC	AAAAAACCAC	5941
CTTGCAAACA	TAATCTGCTG	TTTCTGCGCG	GATCTTCTTG AGATCCTTTT		AAGATCAAAG	5881
CCCCGTAGAA	GAGCGTCAGA	TCGTTCCACT	AAATCCCTTA ACGIGAGTTT		CTCATGACCA	5821
TTTTGATAAT	TGAAGATCCT	TTAATTTAAA AGGATCTAGG		ATTGATTTAA AACTTCATTT	ATTGATTTAA	5761
TATACTTTAG	TCAGACCAAG TTTACTCATA		TGATTAAGCA TTGGTAACTG		GGTGCCTCAC	5701
CGCTGAGATA	ATAGACAGAT	GATGAACGAA	GGCAACTATG	CGGGGAGTCA	ATCTACACGA	5641
GGGTCTCGCG GTATCATTGC AGCACTGGGG CCAGATGGTA AGCCCTCCCG TATCGTAGTT	AGCCCICCC	CCAGATGGTA	AGCACTGGGG	GTATCATTGC	GGGTCTCGCG	5581

Fig. 26 (SEQ ID NO:60) ICT1024 N TERMINUS 553 AA CODING REGION: 1070-2731

Н	TCAATATTGG	CCATTAGCCA	TATTATTCAT	TCAATAITGG CCATTAGCCA TATTAITCAT TGGTTAIATA GCATAAATCA ATATTGGCTA	GCATAAATCA	ATATTGGCTA
61	TIGGCCATIG		ATCTATATCA	CATACGTTGT ATCTATATCA TAATATGTAC ATTTATATTG GCTCATGTCC	ATTTATATTG	GCTCATGTCC
121	AATATGACCG	CCATGTTGGC	ATTGATTATT	AATATGACCG CCATGTTGGC ATTGATTATT GACTAGTTAT TAATAGTAAT CAATTACGGG	TAATAGTAAT	CAATTACGGG
181	GTCATTAGTT	CATAGCCCAT	ATATGGAGTT	GTCATTAGTT CATAGCCCAT ATATGGAGTT CCGCGTTACA TAACTTACGG TAAATGGCCC	TAACTTACGG	TAAATGGCCC
241	GCCTGGCTGA	CCGCCCAACG	GCCIGGCIGA CCGCCCAACG ACCCCCGCCC	ATTGACGTCA	ATTGACGICA ATAATGACGI	ATGTTCCCAT
301	AGTAACGCCA	ATAGGGACTT	TCCATTGACG	AGTAACGCCA ATAGGGACTT TCCATTGACG TCAATGGGTG GAGTATTTAC GGTAAACTGC	GAGTATTTAC	GGTAAACTGC
361	CCACTTGGCA	GTACATCAAG	TGTATCATAT	CCACTIGGCA GTACATCAAG TGTATCATAT GCCAAGTCCG CCCCCTATTG ACGTCAATGA	CCCCCTATTG	ACGTCAATGA
421	CGGTAAATGG	CGGTAAATGG CCCGCCTGGC	ATTATGCCCA	GTACATGACC	GTACATGACC TTACGGGACT	TICCIACITG
481	GCAGTACATC	GCAGTACATC TACGTATTAG	TCATCGCTAT	TACCATGGTG	TACCATGGTG ATGCGGTTTT	GGCAGTACAC
541	CAATGGGCGT	GGATAGCGGT	TTGACTCACG	TIGACTCACG GGGATTICCA AGICTCCACC CCATIGACGI	AGTCTCCACC	CCATTGACGT
601	CAATGGGAGT	TTGTTTTGGC	ACCAAAATCA	CAAIGGGAGI ITGITITGGC ACCAAAAICA ACGGGACIIT CCAAAAIGIC GIAATAACCC	CCAAAATGTC	GTAATAACCC
661	CGCCCCGLIG	ACGCAAATGG	ACGCAAATGG GCGGTAGGCG		TGTACGGTGG GAGGTCTATA	TAAGCAGAGC
721	TCGTTTAGTG	TCGTTTAGTG AACCGTCAGA	TCACTAGAAG		CTTTATTGCG GTAGTTTATC	ACAGTTAAAT
781	TGCTAACGCA	GTCAGTGCTT	CTGACACAAC	TGCTAACGCA GTCAGTGCTT CTGACACAC AGTCTCGAAC TTAAGCTGCA GAAGTTGGTC	TTAAGCTGCA	GAAGTTGGTC
841	GTGAGGCACT	GGGCAGGTAA	GTGAGGCACT GGGCAGGTAA GTATCAAGGT TACAAGACAG	TACAAGACAG	GTTTAAGGAG	ACCAATAGAA
901	ACTGGGCTTG	TCGAGACAGA	TCGAGACAGA GAAGACTCTT	GCGITICIGA TAGGCACCIA		TIGGICTIAC
961	TGACATCCAC	TTTGCCTTTC	TCTCCACAGG	TGACAICCAC TITGCCTITC TCTCCACAGG TGTCCACTCC CAGITCAAIT ACAGCTCTTA	CAGTICAAIT	ACAGCTCTTA

SCICLI	GCAA	GTGCCGGTGC	GCGTATCGCG	GACGGGGCCA	GGTGAGCACC GCGGGGCCGC GACGGGCCA GCGTATCGCG GTGCCGGTGC GCAAGCTCTT	GGTGAGCACC	2101
GGAGGT	GACA	втесеестсс	GCAGCCCAAG	CCGCAGCCCC	GCGGAAGCAG AAGGAGGGCG CCGCAGCCCC GCAGCCCAAG GTGCGGCTCC GACAGGAGGT	GCGGAAGCAG	2041
AGGCTG	AGCG	CTGCCCTTGG AGCGAGGCTG	TTGAGCGCAG CCACCTGATG		CGCAGCGAGC	GGCCCTGGAC	1981
TCACCGGCGG		CAGGCGGACC	ACTGGGAGAA GGCACCGGAG	ACTGGGAGAA	ATCGGAGGCA GCGCTAAAGG	ATCGGAGGCA	1921
TCGAGTCCCC		GATGAAGTTT	CACATACCCG	AAGAGCTGTC	ATCCTCCATG	CCGGGAAGGT	1861
CCTTCTTTGC		CTGGACACAT	CCCCGATGAG	CAACTGATTT	GAGGAGGACA	TAGCTTTCTG	1801
TCACTCCAGC		CGTCGAAGCT	CCGGGCACGG	GCACCTTTCG	GTTAGGGATG	AGGCCGCTCC	1741
CGCTGATGAA		GCGGCCGCAG	TGGCCAAGAT GAGCTTCCGG		CGAGAGTCGG	GCGGCGCAAG	1681
GGCTCCCGCG		GGTTTCCACC	CTCCCGCTCA	CCTTCTCCAG	TCCCTCTGCT	GGGTGCTGCC	1621
CCGTCACGCC		CCACACACTC	CCTGAGTGCC	CTGCGGAAGG	GCAGATGACA	CTTCCGTGTG	1561
GTGGCCGTGC		ದರ್ಧವಾಡಿದ್ದರ	GCATGCAGAA GATCATAGAC		TGCCAGCTGG	CGTGGGGCCA	1501
CCCCACTCTA		GAGACGCCAC	GACCAGCACC	ACGIGICGCI	AGCCAGGACA	GGACCTGCCC	1441
TCCGGGAGCT		CCCCAGGICC	GAAGCTGAAG	AGCGCTACGG	CACTGCAGCC	GAGCATCCGT	1381
GGCAGCGCAA		ACCCAGAAAT	CAGTGACAGC	TGAGCAAGGA	TGGTTTGGAG	GACCGCCGAC	1321
TCCGCAGGGG		ACACAGACCA	GACGTCCATC	TGCAACGCCA	ದಡಿದರಿದರಿದಿದ	TGAGCTCCGG	1261
CACCCCACCA		CACATCTCTT	CGAGACAGCC	GTATGCCAGC	AGGAGTGTGA	GGCTTTCCTG	1201
TGAGGCGACA		CTGCAGCCCC	GCCCAGCTTC	CGGCAGAAGA	GTGCCCCTGA	TCCCTCTGCG	1141
AGCTGGACAT		CCCTGGCTAA	CAAGAAGCCA	GCCTGCAGCG	AGCACGAGCA	CCGCAGGGAC	1081
TGAGGC	TGAC	GAGAATTCCA	GGCTAGCCTC	ACTCACTATA	AGGCTAGAGT ACTTAATACG ACTCACTATA GGCTAGCCTC GAGAATTCCA TGAGTGAGGC	AGGCTAGAGT	1021

CGCCCGGGAG AAGCGGCCGT ATGGGCTGGG CATGGTGGGA CGGCTCACCA ACCGCACCTA CCGCAAGCGC AICGACAGCI ICGICAAGCG CCAGAICGAG GACAIGGACG ACCACAGGCC CITCITCACC TACTGGCTTA CCTTCGTGCA CTCGCTCGTC ACCATCCTAG CCGTGTGCAT CCGCGGGGTC TACGAGAACG TCAAGTACGT GCAGCAGGAG AACTTCTGGA TCGGGCCCAG TGCTGCGGAA CTCGGAGGCC CTCATCCACC TGGGCGCCAA GTTTTCGCCC TGCATGCGCC AGGACCCGCA GGTGCACAGC TTCATTCGCT CGGCGCGCGA GCGCGAGAAG CACTCCGCCT GCTGCGTGCG TCGGGCTGCG TGCAGACCTC GGAGGAGGAG TGCTCGTCCA CGCTGGCAGT GTGGGTGAAG TGGCCCATCC ATCCCAGCGC CCCAGAGCTT GCGGGCCACA AGAGACAGTT TGGCTCTGTC TGCCACCAGG ATCCCAGGTG AGTCGACCCG GGCGGCCGCT TCGAGCAGAC ATGATAAGAT ACATTGATGA GTTTGGACAA ACCACAACTA GAATGCAGTG AAAAAAATGC TITATITIGIG AAAITIGIGA IGCIAIIGCI ITAITITGIAA CCAITAIAAG CIGCAAIAAA CAAGITAACA ACAACAATIG CAITCAITIT AIGITITCAGG ITCAGGGGGA GAIGIGGGAG GTTTTTAAA GCAAGTAAAA CCTCTACAAA TGTGGTAAAA TCGATAAGGA TCCGGGCTGG CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAG CCTGAATGGC GAATGGACGC GCCCTGTAGC GGCGCATTAA GCGCGGGGGG TGTGGTGGTT ACGCGCAGCG TCGCCACGIT CGCCGGCTTT CCCCGTCAAG CTCTAAATCG GGGGCTCCCT TTAGGGTTCC GATITAGAGC TITACGGCAC CICGACCGCA AAAAACITGA ITIGGGIGAI GGIICACGIA TGACCGCTAC ACTIGCCAGC GCCCTAGCGC CCGCTCCTIT CGCTITCTIC CCTICCTITC CTATGGCATC GCGCCCGTGG GCTTCTCGCA GCATGAGACG GTGGACTCGG CAACGACAGG 2161 2221 2341 2281 2401 2461 2521 2581 2641 2881 2941 2701 2761 2821 3001 3061 3121 3241 3181

GIGGCCCAIC GCCCIGAIAG ACGCITITIC GCCCITIGAC GIIGGAGICC ACGIICTITA ATAGIGGACT CITGITCCAA ACTGGAACAA CACTCAACCC TATCTCGGIC TATICITITG ATTTAACAAA TACAATCTGC CGGGCTTGTC TGCTCCGGC ATCCGCTTAC AGACAAGCTG TGACCGTCTC CGGGAGCTGC TATITIAACGC GAATITITAAC AAAATAITAA CGITITACAAI ITCGCCIGAI GCGGIAITIT ICIGAIGCCG CAIAGITAAG CCAGCCCCGA CACCCGCCAA CACCCGCTGA CGCGCCCTGA TITCGGGGAA AIGIGCGCGG AACCCCIAIT IGITIATITI ICTÁAAIACA IICAAAIAIG GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGIT ITCCAAIGAI GAGCACTITT AAAGIICTGC IAIGIGGCGC GGIAITAICC GAATGACTTG ATGTGTCAGA GGTTTTCACC GTCATCACCG AAACGCGCGA GACGAAAGGG CCTCGTGATA CGCCTATITI TATAGGITAA IGTCAIGATA ATAAIGGITI CITAGACGIC AGGIGGCACI TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT AATATTGAAA AAGGAAGAGT TIGCCIICCI GTIGAGTACT CACCAGICAC AGAAAAGCAI CITACGGAIG GCAIGACAGI AAGAGAAITA IGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT GATITIGCCG ATTICGGCCT ATTGGTTAAA AAATGAGCTG CICCTIACGC AICIGIGGG TATTICACAC CGCATAIGGI GCACICTCAG ATGAGTATIC AACATIICCG IGICGCCCII AITCCCIIII IIGCGGCAII CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA ATTTATAAGG 3301 3361 3421 3481 3541 3601 3661 3721 4141 4381 3781 3841 3901 3961 4201 4261 4321 4021 4081

GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGTAGCAA TGGCAACAAC GTTGCGCAAA CTATTAACTG GCGAACTACT TACTCTAGCT TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC ACTTCTGCGC CGCGGTATCA TIGCAGCACT GGGGCCAGAT GGTAAGCCCT CCCGTAICGT AGTTAICTAC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG GAGCCGGTGA GCGTGGGTCT TTAGATTGAT ACGACGGGGA GTCAGGCAAC TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TAATCTCATG ACCAAAATCC CITAACGIGA GITTICGITC CACIGAGCGI CAGACCCCGI AGAAAAAIC AAAGGATCTT CTTGAGATCC TTTTTTTCTG CGCGTAATCT GCTGCTTGCA AACAAAAAA CCACCGCTAC CAGCGGTGGT TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG CCAGIGGCIG CIGCCAGIGG CGAIAAGICG IGICTIACCG GGIIGGACIC AAGACGAIAG GTAACTGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA GGCCACCACT ICAAGAACTC TGTAGCACCG CCTACATACC ICGCTCTGCT AATCCTGTTA TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA ACTGAGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT CGGGTTTCGC CACCICIGAC TIGAGCGICG ATTITIGIGA IGCICGICAG GGGGGCGGAG CCIAIGGAAA CATATATACT TTAAAACTIC AITITTAAIT TAAAAGGAIC TAGGIGAAGA ICCITITIGA TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT 4441 4501 4561 4621 4681 4741 4801 4861 4921 4981 5041 5161 5221 5401 5281 5341

5581 AACGCCAGCA ACGCGGCCTT TTTACGGTTC CTGGCCTTTT GCTGGCCTTT TGCTCACATG

5641 GCTCGACAGA TCT

Fig. 27, (SEQ ID NO: 61) ICT1024 coding region: 947-3518

러	TCGACTCGAG	CGGCCGCATC	GTGACTGACT	GACGATCTGC	TCGACTCGAG CGGCCGCATC GTGACTGACT GACGATCTGC CTCGCGCGTT	TCGGTGATGA
61	CGGTGAAAAC	CTCTGACACA	TGCAGCTCCC	TGCAGCTCCC GGAGACGGTC	ACAGCTTGTC	TGTAAGCGGA
121	TGCCGGGAGC	AGACAAGCCC	GTCAGGGCGC	GTCAGCGGGT	TGCCGGGAGC AGACAAGCCC GTCAGGGCGC GTCAGCGGGT GTTGGCGGGT GTCGGGGCGC	GTCGGGGCGC
181	AGCCATGACC	CAGTCACGTA	GCGATAGCGG	AGCCATGACC CAGTCACGTA GCGATAGCGG AGTGTATAAT	TCTTGAAGAC	GAAAGGGCCT
241	CGTGATACGC	CTATTTTAT	AGGTTAATGT	CATGATAATA	CATGATAATA ATGGTTTCTT	AGACGICAGG
301	TGGCACTTTT	CGGGGAAATG	TGCGCGGAAC	CCCTATTIGE		TTATTTTTCT AAATACATTC
361	AAATATGTAT		GACAATAACC	CCGCTCATGA GACAATAACC CTGATAAATG	CTTCAATAAT ATTGAAAAG	ATTGAAAAG
421	GAAGAGTATG	GAAGAGTATG AGTATTCAAC ATTTCCGTGT	ATTTCCGTGT	CGCCCTTATT	CCCTTTTTG	CGGCATTTTG
481	· CCTTCCTGTT		TTTGCTCACC CAGAAACGCT	GGTGAAAGTA	GGTGAAAGTA AAAGATGCTG	AAGATCAGTT
541	GGGTGCACGA	GTGGGTTACA	TCGAACTGGA	TCTCAACAGC	TCGAACTGGA TCTCAACAGC GGTAAGATCC	TTGAGAGTTT
601	TCGCCCCGAA	GAACGTTTTC	CAATGATGAG	CACTTTTAAA	TCGCCCCGAA GAACGTTTTC CAATGATGAG CACTTTTAAA GTTCTGCTAT GTGGCGCGGT	GTGGCGCGGT
661	ATTATCCCGT	ATTATCCCGT GTTGACGCCG GGCAAGAGCA	GGCAAGAGCA	ACTCGGTCGC	CGCATACACT	ATTCTCAGAA
721	TGACTTGGTT	GAGTACTCAC	CAGTCACAGA	GAGTACTCAC CAGTCACAGA AAAGCATCTT ACGGATGGCA		TGACAGTAAG
781	AGAATTATGC	AGAATTATGC AGTGCTGCCA	TAACCATGAG	TGATAACACT	TGATAACACT GCGGCCAACT TACTTCTGAC	TACTTCTGAC
841	AACGATCGGA	GGACCGAAGG	AGCTAACCGC	TTTTTGCAC	AACGATCGGA GGACCGAAGG AGCTAACCGC TTTTTGCAC AACATGGGGG ATCATGTAAC	ATCATGTAAC
901	TCGCCTTGAT CGTTGGGAAC CGGAGCTGAA	CGTTGGGAAC	CGGAGCTGAA	TGAAGCCATA	CCAAACGACG	AGCGTGACAC
1961	CACGATGCCT	GCAGCAATGG	CAACAACGTT	GCGCAAACTA	CACGATGCCT GCAGCAATGG CAACAACGTT GCGCAAACTA TTAACTGGCG AACTACTTAC	AACTACTTAC

TCTAGCTTCC CGGCAACAAT TAATAGACTG GATGGAGGCG GATAAAGTTG CAGGACCACT TCTGCGCTCG GCCCTTCCGG CTGGCTGGTT TATTGCTGAT AAATCTGGAG CCGGTGAGCG TGGGTCTCGC GGTATCATTG CAGCACTGGG GCCAGATGGT AAGCCCTCCC GTATCGTAGT TATCTACACG ACGGGGAGTC AGGCAACTAT GGATGAACGA AATAGACAGA TCGCTGAGAT AGGIGCCICA CIGATTAAGC ATTGGIAACT GICAGACCAA GITTACTCAI AIAIACTTTA TTTTTGATAA TCTCATGACC AAAATCCCTT AACGIGAGTT TTCGTTCCAC TGAGCGTCAG ACCCCGTAGA AAAGAICAAA GGAICTICIT GAGAICCTTI ITTICIGCGC GIAAICIGCI GCIIGCAAAC AAAAAAACCA CCGCTACCAG CGGTGGTTTG TTTGCCGGAT CAAGAGCTAC CAACTCTTTT TCCGAAGGTA ACTGGCTTCA GCAGAGCGCA GATACCAAAT ACTGTCCTTC TAGTGTAGCC GTAGTTAGGC CACCACTTCA AGAACTCTGT AGCACCGCCT ACATACCTCG CTCTGCTAAT CCIGITACCA GIGGCIGCIG CCAGIGGCGA TAAGICGIGI CITACCGGGI IGGACICAAG ACGATAGTTA CCGGATAAGG CGCAGCGGTC GGGCTGAACG GGGGGTTCGT GCACAGCC CAGCITGGAG CGAACGACCI ACACCGAACI GAGAIACCIA CAGCGIGAGC IAIGAGAAAG CGCCACGCTT CCCGAAGGGA GAAAGGCGGA CAGGTATCCG GTAAGCGGCA GGGTCGGAAC AGGAGAGCGC ACGAGGGAGC TTCCAGGGGG AAACGCCTGG TATCTTTATA GTCCTGTCGG ATGGAAAAAC GCCAGCAACG CGGCCTTTTT ACGGTTCCTG GCCTTTTGCT GGCCTTTTGC GGCGGAGCCT TCACATGTTC TTTCCTGCGT TATCCCCTGA TTCTGTGGAT AACCGTATTA CCGCCTTTGA GATTGAITTA AAACTTCAIT TTTAATTTAA AAGGATCTAG GTGAAGAICC GITICGCCAC CICTGACTIG AGCGICGAIT ITIGIGAIGC ICGICAGGGG 1021 1081 1201 1141 1261 1321 1381 1441 1501 1561 1621 1741 1681 1801 1861 1921 1981 2041 2101

GTGAGCTGAT ACCGCTCGCC GCAGCCGAAC GACCGAGCGC AGCGAGTCAG TGAGCGAGGA TTTCACACCG CATAAATTCC GACACCATCG AATGGTGCAA AACCTTTCGC GGTATGGCAT GATAGCGCCC GGAAGAGAGT CAATTCAGGG TGGTGAATGT GAAACCAGTA ACGTTATACG ATGTCGCAGA GCCACGITIC TGCGAAAACG CGGGAAAAG TGGAAGCGGC GATGGCGGAG CTGAATTACA TTCCCAACCG CGTGGCACAA CAACTGGCGG GCAAACAGTC GTTGCTGATT GGCGTTGCCA CCTCCAGTCT GGCCCTGCAC GCGCCGTCGC AAATTGTCGC GGCGATTAAA TCTCGCGCCG ATCAACTGGG TGCCAGCGTG GTGGTGTCGA TGGTAGAACG AAGCGGCGTC GAAGCCTGTA AAGCGGCGGT GCACAAICII CICGCGCAAC GCGICAGIGG GCIGAICAII AACIAICCGC IGGAIGACCA GGAIGCCAIT GCIGIGGAAG CIGCCIGCAC IAAIGIICCG GCGIIAIIIC IIGAIGICIC TGACCAGACA CCCATCAACA GTATTATTTT CTCCCATGAA GACGGTACGC GACTGGGCGT GGAGCATCTG GTCGCATTGG GTCACCAGCA AATCGCGCTG TTAGCGGGCC CATTAAGTTC TGTCTCGGCG CGTCTGCGTC TGGCTGGCTG GCATAATAT CTCACTCGCA ATCAAATTCA GCCGATAGCG GAACGGGAAG GCGACTGGAG TGCCATGTCC GGTTTTCAAC AAACCATGCA GCCAACGAIC AGAIGGCGCI GGGCGCAAIG CGCGCCAITA CCGAGICCGG GCIGCGCGIT GGIGCGGAIA ICICGGIAGI GGGATACGAC GATACCGAAG ACAGCTCATG TTATATCCCG CCGTTAACCA CCATCAAACA GGATTTTCGC CTGCTGGGGC AAACCAGCGT GGACCGCTTG CTGCAACTCT CTCAGGGCCA AGCGGAAGAG CGCCTGATGC GGTATTTTCT CCTTACGCAT CTGTGCGGTA GTATGCCGGT GTCTTTATC AGACCGTTTC CCGCGTGGTG AACCAGGCCA AATGCTGAAT GAGGGCATCG TTCCCACTGC GATGCTGGTT 2161 2341 2401 2461 2521 2581 2641 2701 2881 3001 3121 3181 3061

GGCGGTGAAG GGCAATCAGC TGTTGCCCGT CTCACTGGTG AAAAGAAAAA CCACCCTGGC GCCCAATACG CAAACCGCCT CTCCCCGCGC GTTGGCCGAT TCATTAATGC AGCTGGCACG ACAGGITICC CGACTGGAAA GCGGGCAGTG AGCGCAACGC AATTAATGTG AGTTAGCTCA CTCATTAGGC ACCCCAGGCT TTACACTTTA TGCTTCCGGC TCGTATGTTG TGTGGAATTG TTCACTGGCC CAACAGITGC GCAGCCIGAA IGGCGAAIGG CGCITIGCCI GGIITICCGGC ACCAGAAGCG GTCGTITTAC AACGICGIGA CTGGGAAAAC CCTGGCGTTA CCCAACTTAA TCGCCTTGCA GCACATCCCC CITICGCCAG CIGGCGTAAT AGCGAAGAGG CCCGCACCGA TCGCCCTICC GTGCCGGAAA GCTGGCTGGA GTGCGATCTT CCTGAGGCCG ATACTGTCGT CGTCCCCTCA AACTGGCAGA TGCACGGTTA CGATGCGCCC ATCTACACCA ACGTAACCTA TCCCATTACG GTCAATCCGC CGTTTGTTCC CACGGAGAAT CCGACGGGTT GTTACTCGCT CACATTTAAT AGCTTATCGA CTGCACGGTG CACCAATGCT TCTGGCGTCA GGCAGCCATC GGAAGCTGTG TTGTATGAGC GTTGATGAAA GCTGGCTACA GGAAGGCCAG ACGCGAATTA TTTTTGATGG CGTTGGAATT GTATGGCTGT GCAGGTCGTA AATCACTGCA TAATTCGTGT CGCTCAAGGC GCACTCCCGT TCTGGATAAT GTTTTTGCG CCGACATCAT AACGGTTCTG GCAAATATTC TGAAATGAGC TGTTGACAAT TAATCATCGG CTCGTATAAT GTGTGGAATT GTGAGCGGAT AACAATTTCA CACAGGAAAC AGTATTCATG TCCCCTATAC TAGGTTATTG GAAAATTAAG GGCCTTGTGC GCGATGAAGG TGATAAATGG CGAAACAAAA AGTTTGAATT GGGTTTTGGAG TTTCCCAATC TGAGCGGATA ACAATTTCAC ACAGGAAACA GCTATGACCA TGATTACGGA AACCCACTCG ACTICITITG GAATAICTIG AAGAAAAAA IGAAGAGCAI 3301 3361 3421 3481 3541 3601 3661 3721 3781 3841 4021 4141 4201 4261 3901 3961 4081 4321 4381

	ביל מ	ししいよるものもんだっと	ATCCTCCAAA ATCGGATCTG ATCGAAGGTC GTGGGATCC CAGG	ATCGGATCTG	ATCCTCCAAA	4921
GGTGGCGACC	CCAGCAAGTA TATAGCATGG CCTTTGCAGG GCTGGCAAGC CACGTTTGGT GGTGGCGACC	GCTGGCAAGC	CCTTTGCAGG	TATAGCATGG	CCAGCAAGTA	4861
TACTTGAAAT	TTTTAAAAA CGTATTGAAG CTATCCCACA AATTGATAAG TACTTGAAAT	CTATCCCACA	CGTATTGAAG	TTTTAAAAAA	AATTAGTTTG	4801
GCGTTCCCAA	TGTATGACGC TCTTGATGTT GTTTTATACA TGGACCCAAT GTGCCTGGAT GCGTTCCCAA	TGGACCCAAT	GTTTTATACA	TCTTGATGTT	TGTATGACGC	4741
GACTTCATGT	TCATAAAACA TATTTAAATG GTGATCATGT AACCCATCCT GACTTCATGT	GTGATCATGT	TATTTAAATG	TCATAAAACA	ATCGTTTATG	4681
ATGTTCGAAG	TIGAAACTCT CAAAGITGAT TITCTTAGCA AGCTACCTGA AATGCTGAAA AIGTTCGAAG	AGCTACCTGA	TTTCTTAGCA	CAAAGTTGAT	TTGAAACTCT	4621
AGTAAAGACT	TTGAAGGAGC GGTTTTGGAT ATTAGATACG GTGTTTCGAG AATTGCATAT AGTAAAGACT	GTGTTTCGAG	ATTAGATACG	GGTTTTGGAT	TTGAAGGAGC	4561
ATTTCAATGC	TAGCTGACAA GCACAACATG TTGGGTGGTT GTCCAAAAGA GCGTGCAGAG ATTTCAATGC	GTCCAAAAGA	TIGGGIGGTI	GCACAACATG	TAGCTGACAA	4501
ATACGTTATA	TICCITATIA TAITGAIGGI GAIGITAAAI TAACACAGIC TAIGGCCAIC AIACGITAIA	TAACACAGTC	GATGTTAAAT	TATTGATGGT		4441

2600
947-
region: 947-2600
553 aa coding
53 aa
terminus
024 N
HGH
: 62)
ED NO
FIG. 28, (SEQ ID NO: 62) ICT1024 N
. 28,
FIG

н	AGCTTATCGA	CTGCACGGTG	CACCAATGCT	AGCITATCGA CTGCACGGTG CACCAATGCT TCTGGCGTCA GGCAGCCATC GGAAGCTGTG	GGCAGCCATC	GGAAGCTGTG
61	GTATGGCTGT	GCAGGTCGTA	AATCACTGCA	GTATGGCTGT GCAGGTCGTA AATCACTGCA TAATTCGTGT CGCTCAAGGC	CGCTCAAGGC	GCACTCCCGT
121	TCTGGATAAT	GTTTTTGCG	CCGACATCAT	AACGGTTCTG	GCAAATATTC	TGAAATGAGC
. 181	TGTTGACAAT	TAATCATCGG	CTCGTATAAT	GTGTGGAATT	GTGAGCGGAT	AACAATTTCA
241	CACAGGAAAC	AGTATTCATG	TCCCCTATAC	TAGGTTATTG	GAAAATTAAG	GGCCTTGTGC
301	AACCCACTCG	ACTICTITIG	GAATATCTTG	ААСАААААТА	TGAAGAGCAT	TTGTATGAGC
361	GCGATGAAGG	TGATAAATGG	CGAAACAAAA	AGTTTGAATT	GGGTTTGGAG	TTTCCCAATC
421	TICCTIAITA	TATTGATGGT	GATGTTAAAT	TAACACAGTC	TATGGCCATC	ATACGTTATA
481	TAGCTGACAA	GCACAACATG	TTGGGTGGTT	GTCCAAAAGA GCGTGCAGAG	GCGTGCAGAG	ATTTCAATGC
541	TTGAAGGAGC	TTGAAGGAGC GGTTTTGGAT ATTAGATACG	ATTAGATACG	GTGTTTCGAG AATTGCATAT		AGTAAAGACT
601	TIGAAACICI	TTGAAACTCT CAAAGTTGAT	TTTCTTAGCA	TTTCTTAGCA AGCTACCTGA AATGCTGAAA	AATGCTGAAA	ATGTTCGAAG
661	ATCGTTTATG	TCATAAAACA	TATTTAAATG	GTGATCATGT	AACCCATCCT (GACTTCATGT
721	TGTATGACGC	TCTTGATGTT	GTTTTATACA	TGGACCCAAT	GTGCCTGGAT (GCGTTCCCAA
781	AATTAGTTTG	TTTTAAAAAA	CGTATTGAAG	CTATCCCACA	AATTGATAAG	TACTTGAAAT
841	CCAGCAAGTA	TATAGCATGG	CCTTTGCAGG	GCTGGCAAGC	CACGITIGGI (GGTGGCGACC
901	ATCCTCCAAA	ATCCTCCAAA ATCGGATCTG	ATCGAAGGTC	GTGGGATCCC	CAGGAATTCC 1	ATGAGTGAGG
961	CCCGCAGGGA	CAGCACGAGC	AGCCTGCAGC	GCAAGAAGCC ACCCTGGCTA	ACCCTGGCTA 1	AAGCTGGACA
1021	Treceretee	GGTGCCCCTG	ACGCCAGAAG	TICCCICIGC GGIGCCCCIG ACGGCAGAAG AGCCCAGCII CCIGCAGCCC		CTGAGGCGAC

AGGCTTTCCT GAGGAGTGTG AGTATGCCAG CCGAGACAGC CCACATCTCT TCACCCCACC ATGAGCTCCG GCGGCCGGTG CTGCAACGCC AGACGTCCAT CACACAGACC ATCCGCAGGG GGACCGCCGA CTGGTTTGGA GTGAGCAAGG ACAGTGACAG CACCCAGAAA TGGCAGCGCA AGAGCATCCG TCACTGCAGC CAGCGCTACG GGAAGCTGAA GCCCCAGGTC CTCCGGGAGC TGGACCTGCC CAGCCAGGAC AACGTGTCGC TGACCAGCAC CGAGACGCCA CCCCCACTCT ACGIGGGCC AIGCCAGCIG GGCAIGCAGA AGAICAIAGA CCCCCIGGCC CGIGGCCGIG GGCAGATGAC ACTGCGGAAG GCCTGAGTGC CCCACACACT CCCGTCACGC AAGGCCGCTC CGTTAGGGAT GGCACCTTTC GCCGGGCACG GCGTCGAAGC TTCACTCCAG CTAGCITICI GGAGGAC ACAACIGAII ICCCCGAIGA GCIGGACACA ICCIICTIIG CGGGTGCTGC CTCCCTCTGC TCCTTCTCCA GCTCCCGCTC AGGTTTCCAC CGGCTCCCGC CATCGGAGGC AGCGCTAAAG GACTGGGAGA AGGCACCGGA GCAGGCGGAC CTCACCGGCG GGCGGCGCAA GCGAGAGTCG GTGGCCAAGA TGAGCTTCCG GGCGGCCGCA GCGCTGATGA CCCGGGAAGG TATCCTCCAT GAAGAGCTGT CCACATACCC GGATGAAGTT TTCGAGTCCC GGCCCTGGA CCGCAGCGAG CTTGAGCGCA GCCACCTGAT GCTGCCCTTG GAGCGAGGCT GGCGGAAGCA GAAGGAGGGC GCCGCAGCCC CGCAGCCCAA GGTGCGGCTC CGACAGGAGG TGGTGAGCAC CGCGGGCCG CGACGGGCC AGCGTATCGC GGTGCCGGTG CGCAAGCTCT CCTTCTTCAC CTACTGGCTT ACCTTCGTGC ACTCGCTCGT CACCATCCTA GCCGTGTGCA TCGCCCGGGA GAAGCGGCCG TAIGGGCTGG GCAIGGTGGG ACGGCTCACC AACCGCACCI ACCGCAAGCG CATCGACAGC TTCGTCAAGC GCCAGATCGA GGACATGGAC GACCACAGGC CCTTCCGTGT 1081 1141 1261 1321 1381 1441 1501 1561 1621 1681 1741 1801 1861 1921 1981 2041 2161 2101

TCTATGGCAT CGCGCCCGTG GGCTTCTCGC AGCATGAGAC GGTGGACTCG GTGCTGCGGA GCAACGACAG GTCGGGCTGC GTGCAGACCT CGGAGGAGGA GTGCTCGTCC ACGCTGGCAG CTACGAGAAC GICAAGIACG IGCAGCAGGA GAACTICTGG AICGGGCCCA CIGCAIGCGC CAGGACCCGC AGGIGCACAG CITCAITCGC ICGGCGCGCG AGCGCGAGAA GCACICCGCC IGCIGCGIGC TGTGGGTGAA GTGGCCCATC CATCCCAGCG CCCCAGAGCT TGCGGGCCAC AAGAGACAGT TIGGCICIGI CIGCCACCAG GAICCCAGGI GAGICGACIC GAGCGGCCGC AICGIGACIG ACTGACGATC TGCCTCGCGC GTTTCGGTGA TGACGGTGAA AACCTCTGAC ACATGCAGCT CCCGGAGACG GTCACAGCTT GTCTGTAAGC GGATGCCGGG AGCAGACAAG CCCGTCAGGG CGCGTCAGCG GGTGTTGGCG GGTGTCGGGG CGCAGCCATG ACCCAGTCAC GTAGCGATAG CGGAGTGTAT AATTCTTGAA GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTTAA CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG TICAAATAIG TAICCGCICA IGAGACAATA ACCCTGATAA ATGCTTCAAT AATATTGAAA AAGGAAGAGT ATGAGTATTC AACATTTCCG GTTTTTGCTC ACCCAGAAAC CACCAGTCAC CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG GTTGAGTACT CGTGTTGACG GCTCGGAGGC CCTCATCCAC CTGGGCGCCA AGTTTTCGCC GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA TGTCGCCCTT ATTCCCTTTT TTGCGGCATT TTGCCTTCCT GAGCACITIT AAAGIICIGC IAIGIGGCGC GGIAITAICC AACCCCTAIT IGITIATITI ICIAAAIACA TGTCATGATA ATAATGGTTT ACCGCGGGGT 2221 2401 2521 2581 2641 2461 2701 2761 2821 2881 3301 3061 3121 3181 3241

GAGTGATAAC ACTGCGGCCA ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA TGCAGTGCTG CCATAACCAT GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA TGGCAACAAC CGCTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT GTTGCGCAAA CTATTAACTG GCGAACTACT TACTCTAGCT TCCCGGCAAC AATTAATAGA GGGCCCAGAT GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGA GTCAGGCAAC CGGCTGGCTG TTGCAGCACT TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGICAGAC CAAGITIACI CAIATAIACI ITAGAITGAI ITAAAACIIC AITITIAAII TAAAAGGATC TAGGTGAAGA TCCTTTTTGA TAATCTCATG ACCAAAATCC CTTAACGTGA CACTGAGCGT CAGACCCCGT AGAAAGATC AAAGGATCTT CTTGAGATCC TITITITICIG CGCGIPATCI GCIGCIIGCA AACAAAAAA CCACCGCIAC CAGCGGIGGI TITICCGAAG GTAACTGGCT TCAGCAGAGC TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG GGTTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG ACTGAGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC GTCGGGCTGA ACGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA CTGGATGGAG GCGGATAAAG TTGCAGGACC ACTTCTGCGC TCGGCCCTTC CGCGGTATCA GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA GGCCACCACT GITTATTGCT GATAAICTG GAGCCGGTGA GCGTGGGTCT TIGITIGCCG GAICAAGAGC IACCAACICI GTTTTCGTTC 3361 3781 3841 3421 3481 3541 3601 3661 3901 3721 3961 4141 4021 4081 4201 4261 4321 4381

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GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC IGGTAICTIT ATAGICCIGI CGGGITICGC CACCICTGAC ITGAGCGICG TGATICIGIG GAIAACCGIA TIACCGCCII IGAGIGAGCI GAIACCGCIC GCCGCAGCCG TITACGGITC CIGGCCITIT GCIGGCCITT IGCICACAIG ITCTITCCIG CGITAICCCC TICCCGCGTG GTGAACCAGG CCAGCCACGI TTCTGCGAAA ACGCGGGAAA AAGTGGAAGC ATITITIGIGA IGCICGICAG GGGGGGGAG CCIATGGAAA AACGCCAGCA ACGCGGCCTI AACGACCGAG CGCAGCGAGT CAGTGAGCGA GGAAGCGGAA GAGCGCCTGA TGCGGTATTT TCGAATGGTG CAAAACCTTT CGCGGTATGG CATGATAGCG CCCGGAAGAG AGTCAATTCA GGGTGGTGAA TGTGAAACCA GTAACGTTAT ACGATGTCGC AGAGTATGCC GGTGTCTCTT ATCAGACCGT GGCGATGGCG GAGCTGAATT ACATTCCCAA CCGCGTGGCA CAACAACTGG CGGGCAAACA ACGAAGCGGC GTCGAAGCCT GTAAAGCGGC GGTGCACAAT CTTCTCGCGC AACGCGTCAG GTCGTIGCIG ATTGGCGTIG CCACCTCCAG TCTGGCCCCTG CACGCGCCGT CGCAAATTGI CGCGGCGATT AAATCTCGCG CCGATCAACT GGGTGCCAGC GTGGTGGTGT CGATGGTAGA TGGGCTGATC ATTAACTATC CGCTGGATGA CCAGGATGCC ATTGCTGTGG AAGCTGCCTG CACTAATGTT CCGGCGTTAT TTCTTGATGT CTCTGACCAG ACACCCATCA ACAGTATTAT TTTCTCCCAT GAAGACGGTA CGCGACTGGG CGTGGAGCAT CTGGTCGCAT TGGGTCACCA GCAAATCGCG CIGITAGCGG GCCCAITAAG ITCIGICICG GCGCGICIGC GICIGGCIGG CTGGCATAAA TATCTCACTC GCAATCAAAT TCAGCCGATA GCGGAACGGG AAGGCGACTG TCTCCTTACG CATCTGTGCG GTATTTCACA CCGCATAAAT TCCGACACCA 4501 4561 4621 4681 4741 4801 4861 4921 4981 5041 5101 5161 5221 5341 5401 5281 5521

CAGACGCGAA TTATTTTTGA TGGCGTTGGA ATT	6601 C2
AATCCGACGG GTTGTTACTC GCTCACATTT AATGTTGATG AAAGCTGGCT ACAGGAAGGC	6541 A
CCCATCTACA CCAACGTAAC CTATCCCATT ACGGTCAATC CGCCGTTTGT TCCCACGGAG	6481 C
CITCCTGAGG CCGATACTGT CGTCGTCCCC TCAAACTGGC AGATGCACGG TTACGATGCG	6421 C
TGGCGCTTTG CCTGGTTTCC GGCACCAGAA GCGGTGCCGG AAAGCTGGCT GGAGTGCGAT	6361 T
AATAGCGAAG AGGCCCGCAC CGATCGCCCT TCCCAACAGT TGCGCAGCCT GAATGGCGAA	6301 A
AACCCIGGCG TTACCCAACT TAATCGCCTT GCAGCACATC CCCCTTTCGC CAGCTGGCGT	6241 A
ACAGCTATGA CCATGATTAC GGATTCACTG GCCGTCGTTT TACAACGTCG TGACTGGGAA	6181 A
TTATGCTTCC GGCTCGTATG TTGTGGGGGGGG ATAACAATTT CACACAGGAA	6121 T
GTGAGCGCAA CGCAATTAAT GTGAGTTAGC TCACTCATTA GGCACCCCAG GCTTTACACT	6061 G
CGCGTTGGCC GATTCATTAA TGCAGCTGGC ACGACAGGTT TCCCGACTGG AAAGCGGGCA	6001 C
CGTCTCACTG GTGAAAAGAA AAACCACCCT GGCGCCCCAAT ACGCAAACCG CCTCTCCCCG	5941 C
CGTGGACCGC TTGCTGCAAC TCTCTCAGGG CCAGGCGGTG AAGGGCAATC AGCTGTTGCC	5881 C
ATGTTATATC CCGCCGTTAA CCACCATCAA ACAGGATTTT CGCCTGCTGG GGCAAACCAG	5821 A
CGGGCTGCGC GTTGGTGCGG ATATCTCGGT AGTGGGATAC GACGATACCG AAGACAGCTC	5761 C
TGCGATGCTG GTTGCCAACG ATCAGATGGC GCTGGGCGCA ATGCGCGCCA TTACCGAGTC	5701 I
GAGTGCCATG TCCGGTTTTC AACAAACCAT GCAAATGCTG AATGAGGGCA TCGTTCCCAC	5641 G

FIG. 29, (SEQ ID NO:64) Coding region for the C terminus 375 aa: 945-2069

Н	AGCTTATCGA	AGCTTATCGA CTGCACGGTG CACCAATGCT TCTGGCGTCA GGCAGCCATC GGAAGCTGTG	CACCAATGCT	TCTGGCGTCA	GGCAGCCATC	GGAAGCTGTG
61	GTATGGCTGT		GCAGGTCGTA AATCACTGCA	TAATTCGTGT	CGCTCAAGGC	CGCTCAAGGC GCACTCCCGT
121	TCTGGATAAT	GITTTTTGCG	CCGACATCAT	AACGGTTCTG	GCAAATATTC	TGAAATGAGC
181	TGTTGACAAT	TAATCATCGG	CTCGTATAAT	GTGTGGAATT	GTGAGCGGAT	AACAATTTCA
241	CACAGGAAAC	AGTATTCATG	TCCCTATAC	TAGGTTATTG	GAAAATTAAG	GGCCTTGTGC
301	AACCCACTCG	ACTTCTTTG	GAATATCTTG	AAGAAAATA	TGAAGAGCAT	TTGTATGAGC
361	GCGATGAAGG	TGATAAATGG		CGAAACAAAA AGITIGAAIT	GGGTTTGGAG	TTTCCCAATC
421	TTCCTTATTA	TATTGATGGT	GATGTTAAAT	TAACACAGTC	TATGGCCATC	ATACGTTATA
481	TAGCTGACAA	GCACAACAIG	TIGGGIGGII		GTCCAAAAGA GCGTGCAGAG ATTTCAATGC	ATTTCAATGC
541	TTGAAGGAGC	GGTTTTGGAT	ATTAGATACG	ATTAGATACG GTGTTTCGAG AATTGCATAT AGTAAAGACT	AATTGCATAT	AGTAAAGACT
601	TTGAAACTCT	CAAAGTTGAT	TTTCTTAGCA	TTTCTTAGCA AGCTACCTGA AATGCTGAAA ATGTTCGAAG	AATGCTGAAA	ATGTTCGAAG
199	ATCGTTTATG	TCATAAAACA	TATTTAAATG	TATITAAAIG GIGAICAIGI AACCCAICCI GACTICAIGI	AACCCATCCT	GACTTCATGT
721	TGTATGACGC	TCTTGATGTT	GTTTTATACA	TGGACCCAAT	GTGCCTGGAT	GCGTTCCCAA
781	AATTAGTTTG	TTTTAAAAAA	CGTATTGAAG		CTATCCCACA AATTGATAAG	TACTTGAAAT
841	CCAGCAAGTA	TATAGCATGG	CCTTTGCAGG	GCTGGCAAGC CACGTTTGGT	CACGTTTGGT	GGTGGCGACC
901	ATCCTCCAAA	ATCCTCCAAA ATCGGATCTG	ATCGAAGGTC	GTGGGATCCC	CAGGAATTCC	CAGGTGCACA
961	GCTTCATTCG	CTCGGCGCGC	GAGCGCGAGA	GAGCGCGAGA AGCACTCCGC	CTGCTGCGTG	CGCAACGACA
1021	GGTCGGGCTG		TCGGAGGAGG	CGTGCAGACC TCGGAGGAGG AGTGCTCGTC CACGCTGGCA	CACGCTGGCA	GTGTGGGTGA

AGIGGCCCAI CCAICCCAGC GCCCCAGAGC TIGCGGGCCA CAAGAGACAG ITIGGCICIG CAGAAGACAT CACCAAGIGG CCGAICIGCA CCAAAAACAG CGCIGGGAAC CACACCAACC GTGAGATCAC CTCCCGGGAG TACTGTGACT TCATGAGGGG CTACTTCCAT GAGGAGGCCA TCTGCCACCA GGATCCCAGG GTGTGTGATG AGCCCTCCTC CGAAGACCCT CATGAGTGGC ATCCCCACAT GGACTGTGTC ATCACAGGAC GGCCCTGCTG CATTGGCACC AAGGGCAGGT CGCICTGCIC ICAGGIGCAC IGCAIGGAIG AIGIGIGIGG GCICCIGCCI ITICICAACC CCGAGGIGCC IGACCAGITC TACCGCCIGI GGCIAICCCI CIICCIGCAC GCCGGGAICI TGCACTGCCT GGTGTCCATC TGCTTCCAGA TGACTGTCCT GCGGGACCTG GAGAAGCTGG CAGGCTGGCA CCGCATAGCC ATCATCTACC TGCTGAGTGG TGTCACCGGC AACCTGGCCA GTGCCATCTT CCTGCCATAC CGAGCAGAGG TGGGTCCTGC TGGCTCCCAG TTCGGCATCC TGGCCTGCCT CTTCGTGGAG CTCTTCCAGA GCTGGCAGAT CCTGGCGCGG CCCTGGCGTG CCTICITCAA GCIGCIGGCI GIGGIGCICI ICCICIICAC CITIGGGCIG CIGCCGIGGA TIGACAACIT IGCCCACAIC ICGGGGIICA ICAGIGGCCI CIICCICICC IICGCCIICI TGCCCTACAT CAGCTTTGGC AAGTTCGACC TGTACCGGAA ACGCTGCCAG ATCATCATCT TICAGGIGGI CIICCIGGGC CICCIGGCIG GCCIGGIGGI CCICIICIAC GICIAICCIG TCCGCTGTGA GTGGTGTGAG TTCCTCACCT GCATCCCCTT CACTGACAG TTCTGTGAGA AGTACGAACT GGACGCTCAG CTCCACTGAG TCGACTCGAG CGGCCGCATC GTGACTGACT GACGATCTGC CTCGCGCGTT TCGGTGATGA CGGTGAAAAC CTCTGACACA TGCAGCTCCC GGAGACGGTC ACAGCTTGTC TGTAAGCGGA TGCCGGGAGC AGACAAGCCC GTCAGGGCGC 1081 1141 1201 1261 1321 1381 1441 1501 1561 1621 1681 1741 1801 1861 1921 2041 2101 2161

GTCAGCGGGT GITGGCGGGT GICGGGCGC AGCCAIGACC CAGICACGIA GCGAIAGCGG CATGATAATA ATGGTTTCTT AGACGTCAGG TGGCACTTTT CGGGGAAATG TGCGCGGAAC CCCTATITGI ITAITITICI AAATACAITC AAAIAIGIAI CCGCICAIGA GACAAIAACC TCTCAACAGC GGTAAGATCC TTGAGAGTTT TCGCCCCGAA GAACGTTTTC CAATGATGAG AGTGTATAAT ICTTGAAGAC GAAAGGGCCT CGTGATACGC CTATTTTAT AGGTTAATGT CTGATAAATG CITCAATAAT AITGAAAAG GAAGAGTATG AGTATTCAAC AITTCCGTGI TCGAACTGGA CACTITIAAA GIICIGCIAI GIGGCGCGGI ATIAICCCGI GIIGACGCCG GGCAAGAGCA ACTCGGTCGC CGCATACACT ATTCTCAGAA TGACTTGGTT GAGTACTCAC CAGTCACAGA AAAGCATCTT ACGGATGGCA TGACAGTAAG AGAATTATGC AGTGCTGCCA TAACCATGAG TGATAACACT GCGGCCAACT TACTTCTGAC AACGATCGGA GGACCGAAGG AGCTAACCGC CGCCCTTATT CCCTTTTTG CGGCATTTTG CCTTCCTGTT TTTGCTCACC CAGAAACGCT TITITIGCAC AACAIGGGGG AICAIGIAAC ICGCCIIGAI CGIIGGGAAC CGGAGCIGAA GCGCAAACTA TTAACTGGCG AACTACTTAC TCTAGCTTCC CGGCAACAAT TAATAGACTG GCCAGAIGGT AAGCCCICCC GIAICGIAGI IAICIACACG ACGGGGAGIC AGGCAACIAI TGAAGCCATA CCAAACGACG AGCGTGACAC CACGATGCCT GCAGCAATGG CAACAACGTT CTGGCTGGTT TATIGCIGAI AAAICIGGAG CCGGIGAGCG IGGGICICGC GGIAICAIIG CAGCACIGGG GGATGAACGA AATAGACAGA TCGCTGAGAT AGGTGCCTCA CTGATTAAGC ATTGGTAACT GGTGAAAGTA AAAGATGCTG AAGATCAGTT GGGTGCACGA GTGGGTTACA GAIGGAGGCG GAIAAAGITG CAGGACCACT ICIGCGCICG GCCCTICCGG 2221 2341 2401 2461 2521 2581 2641 2701 2941 3061 2821 2881 3001 3121 3181 3241 3301

3361		GTTTACTCAT	ATATACTTTA	GICAGACCAA GITTACICAI ATAIACITITA GAITGAITITA AAACITCAIT ITIAAITITAA	AAACTTCATT	TTTAATTTAA
3421	AAGGATCTAG	GTGAAGATCC	TTTTGATAA	TCTCATGACC	AAAATCCCTT	AACGTGAGTT
3481	TTCGTTCCAC	TGAGCGTCAG	ACCCCGTAGA	адасатсада	GGATCTTCTT	GAGATCCTTT
3541	TTTTCTGCGC	GTAATCTGCT	GCTTGCAAAC	ааааааасса	CCGCTACCAG	CGGTGGTTTG
3601	TTTGCCGGAT	CAAGAGCTAC	CAACTCTTTT	TCCGAAGGTA	ACTGGCTTCA	GCAGAGCGCA
3661	GATACCAAAT	ACTGTCCTTC	TAGTGTAGCC	GTAGTTAGGC	CACCACTICA	AGAACTCTGT
3721	AGCACCGCCT	ACATACCTCG	CTCTGCTAAT	CCTGTTACCA	GTGGCTGCTG	CCAGTGGCGA
3781	TAAGTCGTGT	CTTACCGGGT		TGGACTCAAG ACGATAGTTA	CCGGATAAGG	CGCAGCGGIC
3841	GGCTGAACG	GGGGGTTCGT	GCACACAGCC	CAGCTTGGAG	CGAACGACCT	ACACCGAACT
3901	GAGATACCTA	CAGCGTGAGC	TATGAGAAAG	CGCCACGCTT	CCCGAAGGGA	GAAAGGCGGA
3961	CAGGTAICCG	GTAAGCGGCA	GGGTCGGAAC	AGGAGAGCGC	ACGAGGGAGC	TTCCAGGGG
4021	AAACGCCTGG	TATCTTTATA	GTCCTGTCGG	GTTTCGCCAC	CTCTGACTTG	AGCGTCGATT
4081	TITGIGAIGC	TCGTCAGGGG	GGCGGAGCCT	ATGGAAAAC (GCCAGCAACG	CGGCCTTTTT
4141	ACGGTTCCTG	GCCTTTTGCT	GGCCTTTTGC	TCACATGTTC :	TTTCCIGCGI	TATCCCCTGA
4201	TTCTGTGGAT	AACCGTATTA	CCGCCTTTGA	GTGAGCTGAT 1	ACCGCTCGCC GCAGCCGAAC	GCAGCCGAAC
4261	GACCGAGCGC	AGCGAGTCAG	TGAGCGAGGA	TGAGCGAGGA AGCGGAAGAG CGCCTGATGC		GGTATTTTCT
4321	CCTTACGCAT	CTGTGCGGTA	TTTCACACCG	CATAAATTCC (GACACCATCG AATGGTGCAA	AATGGTGCAA
4381	AACCTTTCGC (GGTATGGCAT	GATAGCGCCC GGAAGAGAGT	GGAAGAGAGT (CAATTCAGGG	TGGTGAATGT
4441	GAAACCAGTA ACGTTATACG	ACGTTATACG	ATGTCGCAGA	ATGTCGCAGA GTATGCCGGT GTCTCTTATC		AGACCGTTTC

CCGCGTGGTG AACCAGGCCA GCCACGTTTC TGCGAAAACG CGGGAAAAAG TGGAAGCGGC GCAAACAGTC GTIGCIGAIT GGCGIIGCCA CCICCAGICI GGCCCIGCAC GCGCCGICGC AAAIIGICGC TGGTAGAACG AAGCGGCGTC GAAGCCTGTA AAGCGGCGGT GCACAATCTT CTCGCGCAAC GCGTCAGTGG GCTGATCATT AACTATCCGC TGGATGACCA GGATGCCATT GCTGTGGAAG CTGCCTGCAC TAAIGIICCG GCGIIAITIC ITGAIGICIC IGACCAGACA CCCAICAACA GIAITAITII CTCCCATGAA GACGGTACGC GACTGGGCGT GGAGCATCTG GTCGCALTGG GTCACCAGCA AATCGCGCTG TTAGCGGGCC CATTAAGTTC TGTCTCGGCG CGTCTGCGTC TGGCTGGCTG GCATAAATAT CTCACTCGCA ATCAAATTCA GCCGATAGCG GAACGGGAAG GCGACTGGAG TGCCATGTCC GGTTTTCAAC AAACCATGCA AATGCTGAAT GAGGGCATCG TTCCCACTGC GATECTGGTT GCCAACGATC AGATGGCGCT GGGCGCAATG CGCGCCATTA CCGAGTCCGG GCTGCGCGTT GGTGCGGATA TCTCGGTAGT GGGATACGAC GATACCGAAG ACAGCTCATG CTCCCCGCGC TTATATCCCG CCGTTAACCA CCATCAAACA GGATTTTCGC CTGCTGGGGC AAACCAGCGT GGACCGCTTG CTGCAACTCT CTCAGGGCCA GGCGGTGAAG GGCAATCAGC TGTTGCCCGT GTIGGCCGAI ICAITAAIGC AGCIGGCACG ACAGGIIICC CGACIGGAAA GCGGGCAGIG TGCTTCCGGC TCGTATGTTG TGTGGAATTG TGAGCGGATA ACAATTTCAC ACAGGAAACA TTACACTTTA GATGGCGGAG CTGAATTACA TTCCCAACCG CGTGGCACAA CAACTGGCGG GGCGATTAAA TCTCGCGCCG ATCAACTGGG TGCCAGCGTG GTGGTGTCGA CTCACTGGTG AAAAGAAAAA CCACCCTGGC GCCCAATACG CAAACCGCCT AGCGCAACGC AATTAATGTG AGTTAGCTCA CTCATTAGGC ACCCCAGGCT 4501 4561 4621 4741 4801 4861 4921 4981 5041 5101 5341 5161 5221 5281 5401 5581

			CGTTGGAATT	ACGCGAATTA TTTTTGATGG CGTTGGAATT	ACGCGAATTA	6061
GGAAGGCCAG	CCGACGGGTT GTTACTCGCT CACATTTAAT GTTGATGAAA GCTGGCTACA GGAAGGCCAG	GTTGATGAAA	CACATTTAAT	GTTACTCGCT	CCGACGGGTT	6001
CACGGAGAAT	ATCTACACCA ACGTAACCTA TCCCATTACG GTCAATCCGC CGTTTGTTCC CACGGAGAAT	GTCAATCCGC	TCCCATTACG	ACGTAACCTA	ATCTACACCA	5941
CGATGCGCCC	CCTGAGGCCG ATACTGTCGT CGTCCCCTCA AACTGGCAGA TGCACGGTTA CGATGCGCCC	AACTGGCAGA	CGTCCCCTCA	ATACTGTCGT	CCTGAGGCCG	5881
GTGCGATCTT	CGCTTTGCCT GGTTTCCGGC ACCAGAAGCG GTGCCGGAAA GCTGGCTGGA GTGCGATCTT	GTGCCGGAAA	ACCAGAAGCG	GGTTTCCGGC	CGCTTTGCCT	5821
TGGCGAATGG	AGCGAAGAGG CCCGCACCGA TCGCCCTTCC CAACAGTTGC GCAGCCTGAA TGGCGAATGG	CAACAGTTGC	TCGCCCTTCC	CCCGCACCGA	AGCGAAGAGG	5761
CTGGCGTAAT	CCTGGCGTTA CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG CTGGCGTAAT	GCACATCCCC	TCGCCTTGCA	CCCAACTTAA	CCTGGCGTTA	5701
CTGGGAAAAC	GCTATGACCA TGATTACGGA TTCACTGGCC GTCGTTTTAC AACGTCGTGA CTGGGAAAAC	GTCGTTTTAC	TTCACTGGCC	TGATTACGGA	GCTATGACCA	5641

FIG. 30, (SEQ ID NO:66) ICT1024 coding region: 310-2879

Н	TAATACGACT	TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA TTCCCCTCTA GACTTACAAT	GAATTGTGAG	CGGATAACAA	TTCCCCTCTA	GACTTACAAT
61	TTCCATTCGC	CATTCAGGCT	CATTCAGGCT GCGCAACTGT	TGGGAAGGGC	GATCGGTACG	TGGGAAGGGC GATCGGTACG GGCCTCTTCG
121	CTATTACGCC	CTATTACGCC AGCTTGCGAA CGGTGGTGC GCTGCAAGGC GATTAAGTTG	CGGTGGGTGC	GCTGCAAGGC	GATTAAGTTG	GGTAACGCCA
181	GGATTCTCCC	AGTCACGACG	TTGTAAAACG	TTGTAAACG ACGGCCAGCG	AGAGATCTTG	ATTGGCTAGC
241	AGAATAATTT	TGTTTAACTT	TAAGAAGGAG	ATATACCATG	GCGATATCCC	GGGAGCTCGT
301	GGATCCGAAT	TCCATGAGTG	AGGCCCGCAG	GGACAGCACG	AGCAGCCTGC	AGCGCAAGAA
361	GCCACCCTGG		CTAAAGCTGG ACATTCCCTC	receereccc	CTGACGGCAG	CTGACGGCAG AAGAGCCCAG
421	CTTCCTGCAG	CCCCTGAGGC	GACAGGCTTT	CCTGAGGAGT	GTGAGTATGC	CAGCCGAGAC
481	AGCCCACATC		TCTTCACCCC ACCATGAGCT	ರಾವಾರವಾಕರಾವಾ	GTGCTGCAAC	GCCAGACGTC
541	CATCACACAG	ACCATCCGCA	ACCATCCGCA GGGGGACCGC	CGACTGGTTT GGAGTGAGCA AGGACAGTGA	GGAGTGAGCA	AGGACAGTGA
601	CAGCACCCAG	AAATGGCAGC	AAATGGCAGC GCAAGAGCAT	CCGTCACTGC AGCCAGCGCT ACGGGAAGCT	AGCCAGCGCT	ACGGGAAGCT
199	GAAGCCCCAG	GAAGCCCCAG GICCICCGGG AGCIGGACCI GCCCAGCCAG GACAACGIGI CGCIGACCAG	AGCTGGACCT	GCCCAGCCAG	GACAACGTGT	CGCTGACCAG
721	CACCGAGACG	CACCGAGACG CCACCCCCAC TCTACGTGGG GCCATGCCAG CTGGGCATGC AGAAGATCAT	TCTACGTGGG	GCCATGCCAG	CTGGGCATGC	AGAAGATCAT
781	AGACCCCCTG	AGACCCCTG GCCCGTGGCC GTGCCTTCCG	GTGCCTTCCG	TGTGGCAGAT	GACACTGCGG	AAGGCCTGAG
841	TGCCCCACAC		ACTCCCGTCA CGCCGGGTGC	TGCCTCCCTC TGCTCCTTCT	TGCTCCTTCT	CCAGCTCCCG
901	CTCAGGTTTC	CACCGGCTCC CGCGGCGGCG	ຄວອຄວຄຄວຄວ	CAAGCGAGAG	TCGGTGGCCA	AGATGAGCTT
196	ລລອອລອອລລ	GCAGCGCTGA TGAAAGGCCG	TGAAAGGCCG	CTCCGTTAGG GATGGCACCT		Trecceesec
1021	ACGCCGTCGA	ACGGCGTCGA AGCTTCACTC CAGCTAGCTT TCTGGAGGAG GACACAACTG	CAGCTAGCTT	TCTGGAGGAG	GACACAACTG	ATTTCCCCGA

TGAGCTGGAC ACATCCTTCT TTGCCCGGGA AGGTATCCTC CATGAAGAGC TGTCCACATA CCCGGATGAA GITITCGAGI CCCCATCGGA GGCAGCGCTA AAGGACTGGG AGAAGGCACC GAIGCIGCCC TIGGAGCGAG GCIGGCGGAA GCAGAAGGAG GGCGCCGCAG CCCCGCAGCC GGAGCAGGCG GACCTCACCG GCGGGCCCT GGACCGCAGC GAGCTTGAGC GCAGCCACCT GCCAGCGTAT CGCGGIGCCG GIGCGCAAGC ICTICGCCCG GGAGAAGCGG CCGIAIGGGC IGGGCAIGGI GGGACGCTC ACCAACCGCA CCTACCGCAA GCGCATCGAC AGCTTCGTCA AGCGCCAGAT CGAGGACATG GACGACCACA GGCCCTICTI CACCTACTGG CTTACCTICG TGCACTCGCI CGTCACCATC CTAGCCGTGT GCATCTATGG CATCGCGCCC GTGGGCTTCT CGCAGCATGA GACGGIGGAC ICGGIGCIGC GGAACCGCGG GGICTACGAG AACGICAAGI ACGIGCAGCA GGAGAACTIC IGGAICGGGC CCAGCICGGA GGCCCICAIC CACCIGGGCG CCAAGIIIITC GCCCTGCATG CGCCAGGACC CGCAGGTGCA CAGCTTCATT CGCTCGGCGC GCGAGCGCGA GAAGCACTCC GCCTGCTGCG TGCGCAACGA CAGGTCGGGC TGCGTGCAGA CCTCGGAGGA GGAGTGCTCG TCCACGCTGG CAGTGTGGGT GAAGTGGCCC ATCCATCCCA GCGCCCCAGA GCTIGCGGGC CACAAGAGAC AGTTIGGCTC IGICTGCCAC CAGGAICCCA GGGIGIGIGA TGAGCCCTCC TCCGAAGACC CTCATGAGTG GCCAGAAGAC ATCACCAAGT GGCCGATCTG CACCAAAAAC AGCGCTGGGA ACCACACCAA CCATCCCCAC ATGGACTGTG TCATCACAGG CTTCATGAGG GGCTACTTCC ATGAGGAGGC CACGCTCTGC TCTCAGGTGC ACTGCATGGA ACGGCCCTGC TGCATTGGCA CCAAGGGCAG GTGTGAGATC ACCTCCCGGG AGTACTGTGA CAAGGTGCGG CTCCGACAGG AGGTGGTGAG CACCGCGGGG CCGCGACGGG 1081 1141 1201 1261 1321 1381 1441 1501 1561 1621 1741 1681 1801 1921 1981 2041 1861 2101 2161

TGAIGIGIGI GGGCICCIGC CITITICICAA CCCCGAGGIG CCIGACCAGI ICIACCGCCI CICITCCIGC ACGCCGGGAT CITGCACTGC CIGGIGICCA ICIGCTICCA GGCAGGCTGG CACCGCATAG CCATCATCTA CCTGCTGAGT GGTGTCACCG GCAACCTGGC CAGTGCCATC TTCCTGCCAT ACCGAGCAGA GGTGGGTCCT GCTGGCTCCC AGTTCGGCAT CCTGGCCTGC CTCTTCGTGG AGCTCTTCCA TGGCCTGGTG GICCTCTTCT ACGICTAICC IGICCGCTGI GAGIGGIGIG AGIICCICAC GAGCTGGCAG ATCCTGGCGC GGCCCTGGCG TGCCTTCTTC AAGCTGCTGG CTGTGGTGCT CGCTCCTGAA GACCCAGAGG ATCTCGAGCA CCACCACCAC CACCACTAAT GTTAATTAAG CTICCICIIC ACCITIGGGC IGCIGCCGIG GAIIGACAAC ITIGCCCACA ICICGGGGII GCAAGTTCGA GCCICCIGGC CTGCATCCCC TTCACTGACA AGTTCTGTGA GAAGTACGAA CTGGACGCTC AGCTCCACAT TCGAAGCTIG CGGCCGCACA GCTGTATACA CGTGCAAGCC AGCCAGAACT TIGGGCGTIG TAATCATAGI CATAATCAAT ACTCCTGACT GCGTTAGCAA TTTAACTGIG ATAAACTACC GCATTAAAGC TATTCGATGA TAAGCTGTCA AACATGATAA TTCTTGAAGA CGAAAGGGCC TAGGCTGATA AAACAGAATT TGCCTGGCGG CAGTAGCGCG GTGGTCCCAC CTGACCCCAT GCCGAACTCA GAAGTGAAAC GCCGTAGCGC CGATGGTAGT GTGGGGTCTC CCCATGCGAG AGTAGGGAAC TGCCAGGCAT CAAATAAAAC GAAAGGCTCA GTCGAAAGAC TGGGCCTTTC GITTTATCTG TTGTTTGTCG GTGAACGCTC TCCTGAGTAG GACAAATCCG CATCAGTGGC CTCTTCCTCT CCTTCGCCTT CTTGCCCTAC ATCAGCTTTG CCTGIACCGG AAACGCIGCC AGAICAICAT CTITCAGGIG GICTICCIGG GATGACTGTC CTGCGGGACC TGGAGAAGCT GIGGCIATCC CGATACGCGT 2341 2401 2461 2521 2581 2641 2701 2761 2821 2881 2941 3001 3061 3301 3121 3181 3241

CCGGGAGCGG ATTTGAACGT TGCGAAGCAA CGGCCCGGAG GGTGGCGGGC AGGACGCCCG CCTTTTTGCG TITCTACAAA CICITITGII TAITITICIA AATACAITCA AATAIGIAIC CGCIGAGCAA TAACTAGCAT AACCCCTTGG GGCCTCTAAA CGGGTCTTGA GGGGTTTTTT GCTGAAAGGA GGAACTATAT CCGGATTGGC GAATGGGACG CGCCCTGTAG CGGCGCATTA AGCGCGGCGG GCTCTAAATC GGGGGCTCCC TTTAGGGTTC CGATTTAGTG CTTTACGGCA CCTCGACCCC AAAAACTTG GIGIGGIGGI IACGCGCAGC GIGACCGCIA CACTIGCCAG CGCCCIAGCG CCCGCICCII CGTIGGAGIC CACGIICITI AAIAGIGGAC ICIIGIICCA AACIGGAACA ACACICAACC CTAICTCGGT CTAITCTTIT GAITTATAAG GGAITTTGCC GAITTCGGCC TAITGGTTAA CGCCCTTTGA AAAATGAGCT GATTTAACAA AAATTTAACG CGAATTTTAA CAAAATATTA ACGTTTACAA TITCIGGCGG CACGAIGGCA IGAGAITAIC AAAAAGGAIC IICACCIAGA ICCITITAAA TTAAAAATGA AGTTTTAAAT CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA CCAATGCTTA ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTCGTT CATCCATAGT TGCCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG GGCTTACCAT CTGGCCCCAG TGCTGCAATG ATACCGCGAG ACCCACGCTC ACCGGCTCCA GATTTATCAG CAATAAACCA CCATCCAGTC TATTAATTGT IGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT IGCGCAACGT CCATAAACTG CCAGGCATCA AATTAAGCAG AAGGCCATCC TGACGGATGG TCGCITTICIT CCCTICCITI CICGCCACGI ICGCCGGCII ICCCCGICAA ATTAGGGTGA TGGTTCACGT AGTGGGCCAT CGCCCTGATA GACGGTTTTT GCCAGCCGGA AGGCCGAGG GCAGAAGTGG TCCTGCAACT TTATCCGCCT 3361 3421 3541 3481 3601 3661 3721 3781 3841 3901 4081 4141 4201 3961 4021 4261 4321 4441 4381

4501	TGTTGCCATT	GCTACAGGCA	TCGIGGIGIC	TGTTGCCAIT GCTACAGGCA TCGTGGTGT ACGCTCGTCG TTTGGTATGG	TTTGGTATGG	CTTCATTCAG
4561	CTCCGGTTCC	CAACGATCAA	GGCGAGTTAC	ATGATCCCCC	ATGTTGTGCA	AAAAAGCGGT
4621	TAGCTCCTTC	GGTCCTCCGA	TCGTTGTCAG	AAGTAAGTTG	GCCGCAGTGT	TATCACTCAT
4681	GGTTATGGCA	GCACTGCATA	ATTCTCTTAC	TGTCATGCCA	TCCGTAAGAT	GCTTTTCTGT
4741	GACTGGTGAG		TACTCAACCA AGTCATTCTG	AGAATAGTGT	ATGCGGCGAC	CGAGITGCIC
4801	TECCCGGCG	TCAATACGGG	ATAATACCGC	GCCACATAGC	AGAACTTTAA	AAGTGCTCAT
4861	CATTGGAAAA	CGTTCTTCGG	GGCGAAAACT	CTCAAGGATC	TTACCGCTGT	TGAGATCCAG
4921	TTCGATGTAA	CCCACTCGTG	CACCCAACTG	ATCTTCAGCA	TCTTTTACTT	TCACCAGCGT
4981	TTCTGGGTGA	GCAAAAACAG	GAAGGCAAAA	TGCCGCAAAA	AAGGGAATAA	GGGGGACACG
5041	GAAATGTTGA	ATACTCATAC	TCTTCCTTT	TCAATCATGA	CCAAAATCCC	TTAACGTGAG
5101	TITICGIICC	ACTGAGCGTC	AGACCCCGTA	GAAAAGATCA AAGGATCTTC	AAGGATCTTC	TIGAGAICCI
5161	TTTTTGGC	GCGTAATCTG	CTGCTTGCAA	ACAAAAAAC	CACCGCTACC	AGCGGTGGTT
5221	TGTTTGCCGG	ATCAAGAGCT	ACCAACTCTT	TTTCCGAAGG	TAACTGGCTT	CAGCAGAGCG
5281	CAGATACCAA	ATACTGTCCT	TCTAGTGTAG	CCGTAGTTAG	GCCACCACTT	CAAGAACICT
5341	GTAGCACCGC	CTACATACCT	CGCTCTGCTA	ATCCTGTTAC	CAGTGGCTGC	TGCCAGTGGC
5401	GATAAGTCGT	GTCTTACCGG	GTTGGACTCA	AGACGATAGT	TACCGGATAA	GGCGCAGCGG
5461	TCGGGCTGAA	CGGGGGTTC	GTGCACACAG	CCCAGCTTGG	AGCGAACGAC	CTACACCGAA
5521	CTGAGATACC	TACAGCGTGA	GCTATGAGAA	AGCGCCACGC	TTCCCGAAGG	GAGAAAGGCG
5581	GACAGGTATC	CGGTAAGCGG	CAGGGTCGGA	CGGTAAGCGG CAGGGTCGGA ACAGGAGGG GCACGAGGGA GCTTCCAGGG	GCACGAGGGA	GCTTCCAGGG

GAAAT

6181

	AACGICCCGC	TGCGGCGACG ACCGGTGAAT TGTGAGCGCT CACAATTCTC GTGACATCAT AACGTCCCGC	CACAATTCTC	TGTGAGCGCT	ACCGGTGAAT	TGCGGCGACG	6121
	CAGTCATAAG	GACCCAGAGC GCTGCCGGCA CCTGTCCTAC GAGTTGCATG ATAAAGAAGA CAGTCATAAG	GAGTTGCATG	CCTGTCCTAC	GCTGCCGGCA	GACCCAGAGC	1909
-	CGCCGAAAAT	TACCGCAAGC GACAGGCCGA TCATCGTCGC GCTCCAGCGA AAGCGGTCCT CGCCGAAAT	GCTCCAGCGA	TCATCGTCGC	GACAGGCCGA	TACCGCAAGC	6001
	AGATTCCGAA	GAAACGTTTG GTGGCGGGAC CAGTGACGAA GGCTTGAGCG AGGGCGTGCA AGATTCCGAA	GGCTTGAGCG	CAGTGACGAA	GTGGCGGGAC	GAAACGTTTG	5941
	GCTTCTCGCC	ACGACCGAGC GCAGCGAGTC AGTGAGCGAG GAAGCCGGCG ATAATGGCCT GCTTCTCGCC	GAAGCCGGCG	AGTGAGCGAG	GCAGCGAGTC	ACGACCGAGC	5881
	CCGCAGCCGA	GAITCIGIGG ATAACCGIAI TACCGCCIIT GAGIGAGCIG ATACCGCICG CCGCAGCCGA	GAGTGAGCTG	TACCGCCTTT	ATAACCGTAT	GATTCTGTGG	5821
	GTTAICCCCT	TTACGGTICC IGGCCTTTIG CIGGCCTTTI GCICACAIGI ICTITCCIGC GITAICCCCI	GCTCACATGT	CTGGCCTTTT	TGGCCTTTTG	TIACGGTTCC	5761
	CGCGGCCTTT	TITITGIGAI GCICGICAGG GGGGGGGAGC CIAIGGAAAA ACGCCAGCAA CGCGGCCIITI	CTATGGAAAA	GGGGCGGAGC	GCTCGTCAGG	TTTTTGTGAT	5701
	TGAGCGTCGA	GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA	GGGTTTCGCC	TAGTCCTGTC	GGTATCTTTA	GGAAACGCCT	5641

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3. 31, (SEQ ID NO:68) Coding region for	
IG. 31, (SEQ ID NO:68) Coding region for	
FIG. 31, (SEQ ID NO:68) Coding region for	

н	TAATACGACT	CACTATAGGG	GAATTGTGAG	CGGATAACAA	TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA TTCCCCTCTA GACTTACAAT	GACTTACAAT
61	TTCCATTCGC	CATTCAGGCT	GCGCAACTGT	TGGGAAGGGC GATCGGTACG	GATCGGTACG	GGCCTCTTCG
121	CTATTACGCC	CTATTACGCC AGCTTGCGAA	CGGTGGGTGC	CGGIGGGIGC GCIGCAAGGC	GATTAAGTTG	GGTAACGCCA
181	GGATTCTCCC	GGATTCTCCC AGTCACGACG	TTGTAAAACG	ACGCCCAGCG	AGAGATCTTG 1	ATTGGCTAGC
241	AGAATAATTT	TGTTTAACTT	TAAGAAGGAG	ATATACCATG	GCGATATCCC (GGGAGCTCGT
301	GGATCCGAAT	TCCATGAGTG	AGGCCCGCAG	GGACAGCACG	AGCAGCCTGC 1	AGCGCAAGAA
361	GCCACCCTGG	CTAAAGCTGG	ACATTCCCTC	тесевтессс	CTGACGGCAG A	AAGAGCCCAG
421	CTTCCTGCAG		CCCCTGAGGC GACAGGCTTT	CCTGAGGAGT	GTGAGTATGC (CAGCCGAGAC
481	AGCCCACATC	TCTTCACCCC	TCTTCACCCC ACCATGAGCT	ರಿದಿರಿಕಿರಿದಿರಿ	GTGCTGCAAC GCCAGACGTC	SCCAGACGIC
541	CATCACACAG	ACCATCCGCA	CATCACACAG ACCATCCGCA GGGGGACCGC		CGACTGGITT GGAGTGAGCA AGGACAGTGA	AGGACAGTGA
601	CAGCACCCAG	AAATGGCAGC	CAGCACCCAG AAATGGCAGC GCAAGAGCAT	CCGTCACTGC	CCGTCACTGC AGCCAGCGCT ACGGGAAGCT	ACGGGAAGCT
661	GAAGCCCCAG	GTCCTCCGGG	GAAGCCCCAG GICCICCGGG AGCIGGACCI	GCCCAGCCAG	GACAACGIGT (CGCTGACCAG
721	CACCGAGACG	CACCGAGACG CCACCCCAC	TCTACGTGGG	GCCATGCCAG	CTGGGCATGC A	AGAAGATCAT
781	AGACCCCTG	GCCCGTGGCC	GTGCCTTCCG	TGTGGCAGAT	GACACTGCGG AAGGCCTGAG	AGGCCTGAG
841	TGCCCCACAC	ACTCCCGTCA	CGCCGGGTGC	TGCCTCCCTC '	TGCTCCTTCT C	CCAGCTCCCG
901	CTCAGGTTTC	CACCGGCTCC	වටවවටවට	CAAGCGAGAG	TCGGTGGCCA AGATGAGCTT	GATGAGCTT
1961	ວວອອວອອອວວ	GCAGCGCTGA	TGAAAGGCCG	CTCCGTTAGG (GATGGCACCT I	TTCGCCGGGC
1021	ACGGCGTCGA AGCTTCACTC	AGCTTCACTC	CAGCTAGCTT	TCTGGAGGAG GACACAACTG	GACACAACTG A	ATTTCCCCGA

GTATCCGCTG AGCAAAACT AGCATAACCC CTTGGGGCCT CTAAACGGGT CTTGAGGGGT	2161 (
GAIGGCCTIT ITGCGITTCI ACAAACTCTI ITGITTAITI ITCIAAAIAC AITCAAAIAI	2101
CGGGCAGGAC GCCCCCATA AACTGCCAGG CATCAAATTA AGCAGAAGGC CATCCTGACG	2041
AGTAGGACAA ATCCGCCGGG AGCGGATTTG AACGTTGCGA AGCAACGGCC CGGAGGGTGG	1981
GCTCAGTCGA AAGACTGGGC CTTTCGTTTT ATCTGTTGTT TGTCGGTGAA CGCTCTCCTG	1921
GTAGTGTGGG GTCTCCCCAT GCGAGAGTAG GGAACTGCCA GGCATCAAAT AAAACGAAAG	1861
GCGCGGTGGT CCCACCTGAC CCCATGCCGA ACTCAGAAGT GAAACGCCGT AGCGCCGATG	1801
GATAATTCTT GAAGACGAAA GGGCCTAGGC TGATAAAACA GAATTTGCCT GGCGGCAGTA	1741
AGCAATTTAA CTGTGATAAA CTACCGCATT AAAGCTATTC GATGATAAGC TGTCAAACAT	1681
CTAATGTTAA TTAAGTTGGG CGTTGTAATC ATAGTCATAA TCAATACTCC TGACTGCGTT	1621
AAGCCAGCCA GAACTCGCTC CTGAAGACCC AGAGGATCTC GAGCACCACC ACCACCAC	1561
CGAGGACATG GACATCGATA CGCGTTCGAA GCTTGCGGCC GCACAGCTGT ATACACGTGC	1501
GGGACGGCTC ACCAACCGCA CCTACCGCAA GCGCATCGAC AGCTTCGTCA AGCGCCAGAT	1441
CGCGGTGCCG GTGCGCAAGC TCTTCGCCCG GGAGAAGCGG CCGTATGGGC TGGGCATGGT	1381
CAAGGIGCGG CICCGACAGG AGGIGGIGAG CACCGCGGGG CCGCGACGGG GCCAGCGIAI	1321
GATGCTGCCC TTGGAGCGAG GCTGGCGGAA GCAGAAGGAG GGCGCCGCAG CCCCGCAGCC	1261
GGAGCAGGCG GACCTCACCG GCGGGCCCT GGACCGCAGC GAGCTTGAGC GCAGCCACCT	1201
CCCGGATGAA GTTTTCGAGT CCCCATCGGA GGCAGCGCTA AAGGACTGGG AGAAGGCACC	1141
TGAGCIGGAC ACAICCTICI IIGCCCGGGA AGGIAICCIC CAIGAAGAGC IGICCACAIA	1081

AGTGTTATCA CTCATGGTTA TGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGT	3301 AGTG	
GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC	3241 GTGC	
TAIGGCITCA IICAGCICCG GIICCCAACG AICAAGGCGA GIIACAIGAI CCCCCAIGII	3181 TATG	
TAGITIGCGC AACGITGIIG CCAIIGCIAC AGGCAICGIG GIGICACGCI CGICGIIIGG	3121 TAGT	
CGCCTCCATC CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA	3061 CGCC	
ATCAGCAATA AACCAGCCAG CCGGAAGGGC CGAGCGCAGA AGTGGTCCTG CAACTTTATC	3001 ATCA	
ACCAICTGGC CCCAGTGCTG CAATGATACC GCGAGACCCA CGCTCACCGG CTCCAGATTT	2941 ACCA'	
TCGTTCATCC ATAGTTGCCT GACTCCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT	2881 TCGT	
TTGGTCTGAC AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT	2821 TTGG	
CTAGATCCTT TTAAATTAAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC	2761 CTAG	
TATTAACGTT TACAATTTCT GGCGGCACGA TGGCATGAGA TTATCAAAAA GGATCTTCAC	2701 TATT	
CGGCCTATTG GTTAAAAAAT GAGCTGATTT AACAAAATT TAACGCGAAT TTTAACAAAA	2641 CGGC	
GAACAACACT CAACCCTATC TCGGTCTATT CTTTTGATTT ATAAGGGATT TTGCCGATTT	2581 GAAC	
TITITICGCCC TITGACGITG GAGICCACGI ICTITAAIAG IGGACTCITG ITCCAAACIG	2521 TTTT	
ACCCCAAAAA ACTTGATTAG GGTGATGGTT CACGTAGTGG GCCATCGCCC TGATAGACGG	2461 ACCC	
GTCAAGCTCT AAATCGGGGG CTCCCTTTAG GGTTCCGATT TAGTGCTTTA CGGCACCTCG	2401 GTCA	
TAGCGCCCGC TCCTTCGCT TTCTTCCCTT CCTTTCTCGC CACGTTCGCC GGCTTTCCCC	2341 TAGC	
CATTAAGCGC GGCGGGTGTG GTGGTTACGC GCAGCGTGAC CGCTACACTT GCCAGCGCCC	2281 CATT	
TTTTTGCTGA AAGGAGGAAC TATATCCGGA TTGGCGAATG GGACGCGCCC TGTAGCGGCG	2221 TTT	

AAGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG TGCTCTTGCC CGGCGTCAAT ACGGGATAAT ACCGCGCCAC ATAGCAGAAC CTCATCATTG GAAAACGTTC TTCGGGGCGA AAACTCTCAA GGATCTTACC AATAAGGGCG ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT CATGACCAAA GCTGTTGAGA TCCAGITCGA TGTAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTTT CAAAAAAGGG TCTTCTTGAG ATCCTTTTTT TCTGCGCGTA ATCTGCTGCT TGCAAACAAA AAAACCACCG ATCCCTTAAC GTGAGTTTTC GTTCCACTGA GCGTCAGACC CCGTAGAAA GATCAAAGGA GGCTTCAGCA GAGCGCAGAT ACCAAATACT GTCCTTCTAG TGTAGCCGTA GTTAGGCCAC CACTICAAGA ACTCIGIAGC ACCGCCIACA TACCICGCIC IGCIAAICCI GITACCAGIG GAAGGTAACT GCTGCTGCCA GTGGCGATAA GTCGTGTTT ACCGGGTTGG ACTCAAGACG ATAGTTACCG GATAAGGCGC AGCGGTCGGG CTGAACGGGG GGTTCGTGCA CACAGCCCAG CTTGGAGCGA ACGACCTACA CCGAACTGAG ATACCTACAG CGTGAGCTAT GAGAAAGCGC CACGCTTCCC GAAGGGAGAA AGGCGGACAG GTATCCGGTA AGCGGCAGGG TCGGAACAGG AGAGCGCACG AGGGAGCTIC CAGGGGGAAA CGCCTGGTAT CTTTATAGTC CTGTCGGGTT TCGCCACCTC CCIGCGITAI CCCCIGAITC IGIGGAIAAC CGIAITACCG CCITIGAGIG AGCIGAIACC GAAAAACGCC AGCAACGCGG CCTITITACG GTICCTGGCC TTTTGCTGGC CTTTTGCTCA CATGITCTTT TACTITCACC AGCGITICIG GGIGAGCAAA AACAGGAAGG CAAAAIGCCG CTCTTTTCC TGACTIGAGC GICGAITITI GIGAIGCICG ICAGGGGGGC GGAGCCIAIG CTACCAGCGG IGGITIGITT GCCGGAICAA GAGCIACCAA GCGACCGAGT TTTAAAAGTG 3361 3421 3541 3481 3601 3721 3781 3841 3901 3961 4021 4141 4201 4321 4081 4381 4441

				CCCGCGAAAT	ATCATAACGT CCCGCGAAAT	4801
TTCTCGTGAC	GCGCTCACAA	TGAATTGTGA	CGACGACCGG	ATAAGTGCGG	GAAGACAGTC ATAAGTGCGG CGACGACCGG TGAATTGTGA GCGCTCACAA TTCTCGTGAC	4741
GCATGATAAA	CCTACGAGTT	CGGCACCTGT	AGAGCGCTGC	AAAATGACCC	GICCICGCCG AAAAIGACCC AGAGCGCIGC CGGCACCIGI CCIACGAGII GCAIGAIAAA	4681
AGCGAAAGCG	Greecerce	GCCGATCATC	CAAGCGACAG	CCGAATACCG	GTGCAAGATT CCGAATACCG CAAGCGACAG GCCGATCATC GTCGCGCTCC AGCGAAAGCG	4621
GAGCGAGGGC	ACGAAGGCTT	GGGACCAGTG	GTTTGGTGGC	TCGCCGAAAC	GGCCTGCTTC TCGCCGAAAC GTTTGGTGGC GGGACCAGTG ACGAAGGCTT GAGCGAGGGC	4561
CGGCGATAAT	GCGAGGAAGC	GAGTCAGTGA	CGAGCGCAGC	GCCGAACGAC	4501 GCTCGCCGCA GCCGAACGAC CGAGCGCAGC GAGTCAGTGA GCGAGGAAGC CGGCGATAAT	4501

FIG. 32, (SEQ ID NO 69) Coding region for the C terminus 373 aa of ICT1024: 308-1431

ACAAT	CTTCG	GGTAACGCCA	CTAGC	CTCGT	CACTC	IGCIC	3000	CCTC	чаааа	CCTG	ATGAG	FIGIG	TATC	CTGT	TGAG	GTCC	GGCA
GACTT	GGCCTCTTCG		ATTGGCTAGC	GGGAGCTCGT	AGAAG	AGGAG	AGCTT	ATGAG	GCACC	GACGG	ACTTC	ATGATGTGTG	TGTGGCTATC	AGATGACTGT	ACCTGCTGAG	AGGTGGGTCC	AGAGCI
TICCCCICIE	TGGGAAGGGC GATCGGTACG	GCTGCAAGGC GATTAAGTTG	AGAGATCTTG	GCGATATCCC	CGCGAGCGCG AGAAGCACTC	ACCICGGAGG AGGAGIGCTC	CATCCATCCC AGCGCCCCAG AGCTTGCGGG	CCAGGATCCC AGGGTGTGTG ATGAGCCCTC	TGGCCGATCT GCACCAAAAA	GTCATCACAG	GAGTACTGTG	CACTGCATGG	TTCTACCGCC	ATCTGCTTCC	GCCATCATCT	TACCGAGCAG	GAGCTCTTCC
CGGATAACAA		GCTGCAAGGC	TIGIAAAACG ACGGCCAGCG AGAGAICIIG	ATATACCATG	rcecrceece	CTGCGTGCAG			CATCACCAAG	CATGGACTGT	CACCTCCCGG	CICICAGGIG CACTGCAIGG	GCCTGACCAG	CCTGGTGTCC	GCACCGCATA	CITCCTGCCA	CCICIICGIG GAGCICIICC AGAGCIGGCA
GAATTGTGAG	GCGCAACTGT	CGGTGGGTGC	TTGTAAAACG	Taagaaggag	ACAGCTTCAT	ACAGGTCGGG	TGAAGTGGCC	CTGTCTGCCA	GGCCAGAAGA	ACCATCCCCA	GGTGTGAGAT	CATGAGGAGG CCACGCTCTG	ACCCCGAGGT	TCTTGCACTG	TGGCAGGCTG	CCAGTGCCAT	TCCTGGCCTG
TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA TTCCCCTCTA GACTTACAAT	CATTCAGGCT	CTATTACGCC AGCTTGCGAA CGGTGGGTGC	GGATTCTCCC AGTCACGACG	TGTTTAACTT	TCCCAGGTGC	GTGCGCAACG	GCAGTGTGGG	CAGTTTGGCT	CCTCATGAGT	AACCACACCA ACCATCCCCA CATGGACTGT GTCATCACAG GACGGCCCTG	ACCAAGGGCA GGTGTGAGAT CACCTCCCGG GAGTACTGTG ACTTCATGAG	CATGAGGAGG	CCTTTTCTCA ACCCCGAGGT GCCTGACCAG	CACGCCGGGA	CTGGAGAAGC	GGCAACCTGG	CAGTTCGGCA
TAATACGACT	TTCCATTCGC	CTATTACGCC	GGATTCTCC	AGAATAATTT	GGATCCGAAT	CGCCTGCTGC	GTCCACGCTG	CCACAAGAGA	CTCCGAAGAC	CAGCGCTGGG	CTGCATTGGC	GGGCTACTTC	TGGGCTCCTG	CCTCTTCCTG	CCTGCGGGAC	TGGTGTCACC	TGCTGGCTCC
7	61	121	181	241	301	361	421	481	541	601	199	721	781	841	901	1961	1021

GAICCIGGCG CGGCCCIGGC GIGCCIICII CAAGCIGCIG GCIGIGGIGC ICIICCICII CACCITIGGG CIGCIGCCGI GGAIIGACAA CITIGCCCAC AICICGGGGI ICAICAGIGG TCTTGCCCTA CATCAGCTTT GGCAAGTTCG ACCTGTACCG CTTCACTGAC AAGTTCTGTG AGAAGTACGA ACTGGACGCT CAGCTCCACA TCGATACGCG GAAACGCTGC CAGATCATCA TCTTTCAGGT GGTCTTCCTG GGCCTCCTGG CTGGCCTGGT GGTCCTCTTC TACGTCTATC CTGTCCGCTG TGAGTGGTGT GAGTTCCTCA CCTGCATCCC TICGAAGCIT GCGGCCGCAC AGCIGIATAC ACGIGCAAGC CAGCCAGAAC ICGCICCIGA AGACCCAGAG GAICICGAGC ACCACCACCA CCACCACTAA IGITAAITAA GIIGGGCGII GTAATCATAG TCATAATCAA TACTCCTGAC TGCGTTAGCA ATTTAACTGT GATAAACTAC CGCATTAAAG CTATTCGATG ATAAGCTGTC AAACATGATA ATTCTTGAAG ACGAAAGGGC CTAGGCTGAT AAAACAGAAT TTGCCTGGCG GCAGTAGCGC GGTGGTCCCA CCTGACCCCA TGCCGAACTC AGAAGTGAAA CGCCGTAGCG CCGATGGTAG TGTGGGGTCT CCCCATGCGA CGITITATCI GITGITIGIC GGIGAACGCI CICCIGAGIA GGACAAAICC GCCGGGAGCG GAGTAGGGAA CTGCCAGGCA TCAAATAAAA CGAAAGGCTC AGTCGAAAGA CTGGGCCTTT GATITIGAACG ITGCGAAGCA ACGGCCCGGA GGGTGGCGGG CAGGACGCCC GCCATAAACT GCCAGGCAIC AAATTAAGCA GAAGGCCAIC CIGACGGAIG GCCITITIGC GITICIACAA ACTCTTTTGT TTATTTTTCT AAATACATTC AAATATGTAT CCGCTGAGCA ATAACTAGCA TAACCCCTTG GGGCCTCTAA ACGGGTCTTG AGGGGTTTTT TGCTGAAAGG AGGAACTATA TCCGGATTGG CGAATGGGAC GCGCCCTGTA GCGGCGCATT AAGCGCGGCG GGTGTGGTGG CCICITCCIC ICCITCGCCI 1081 1141 1441 1261 1321 1381 1501 1561 1621 1741 1681 1801 1861 1921 1981 2041 2101 2161

TTACGCGCAG CGTGACCGCT ACACTTGCCA GCGCCCTAGC GCCCGCTCCT TTCGCTTTCT TCCCITCCIT ICTCGCCACG TTCGCCGGCT TTCCCCGTCA AGCTCTAAAT CGGGGGCTCC GATTAGGGTG CCACGITCII IAAIAGIGGA CICIIGIICC AAACIGGAAC AACACICAAC CCIAICICGG ICTATICITI IGATITIATAA GGGATITIGC CGATITICGGC CTATIGGITA AAAAAIGAGC TGATITAACA AAAATITAAC GCGAATITIA ACAAAATAIT AACGITTACA AITICIGGCG GCACGATGGC ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTAA ATTAAAAATG ATGGTTCACG TAGTGGGCCA TCGCCCTGAT AGACGGTTTT TCGCCCTTTG ACGTTGGAGT AAGTTTTAAA TCAATCTAAA GTATATGA GTAAACTTGG TCTGACAGTT ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCGT TCATCCATAG TTGCCTGACT CCCCGTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGAITTATCA GCAATAAACC AGCCAGCCGG AAGGGCCGAG CGCAGAAGIG GICCIGCAAC ITTAICCGCC ICCAICCAGI CIAITAAIIG TIGCCGGGAA GCTAGAGTAA GTAGIICGCC AGITAATAGI TIGCGCAACG ITGIIGCCAI TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA GCTCCGGTTC TGGTTATGGC AGCACTGCAT AATICTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG TGACTGGTGA TTAGCTCCTT GTACTCAACC AAGTCATTCT GAGAATAGTG TAIGCGGCGA CCGAGTIGCT CTIGCCCGGC CCGATITAGT GCTITACGGC ACCTCGACCC CAAAAACTT CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG CGGTCCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA CTTTAGGGTT 2221 2341 2401 2461 2521 2581 2641 2701 2761 2821 2941 3001 3061 3181 3241 3301 3121

GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA TCATTGGAAA GTTCGATGTA TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC GGAAATGTTG AATACTCATA CTCTTCCTTT TTCAATCATG ACCAAAATCC CTTAACGTGA GTTTTCGTTC CACTGAGCGT CAGACCCCGT AGAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTTTCTG TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAACTGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG GGTTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA ACTGAGATAC CCGGTAAGCG GCAGGGTCGG AACAGGAGG CGCACGAGGG AGCTTCCAGG GGGAAACGCC CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC GGACAGGTAT TGGTATCTTT ATAGTCCTGT CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG GGGGGGGAG CCTAIGGAAA AACGCCAGCA ACGCGGCCIT ITIACGGIIC CIGGCCTITI GCTGGCCTTT TGCTCACATG TTCTTTCCTG CGTTATCCCC TGATTCTGTG TTACCGCCTT TGAGTGAGCT GATACCGCTC GCCGCAGCCG AACGACCGAG CGCAGCGAGT CAGTGAGCGA GGAAGCCGGC GATAATGGCC TGCTTCTCGC CGAAACGTTT ACGITCTICG GGGCGAAAAC ICTCAAGGAI CITACCGCIG IIGAGAICCA TTCACCAGCG CGCGTAATCT GCTGCTTGCA AACAAAAAA CCACCGCTAC CAGCGGTGGT ACCCACTCGT GCACCCAACT GATCTTCAGC ATCTTTTACT GATAACCGTA 3361 3421 3481 3541 3601 3661 3721 4021 3781 3841 3901 3961 4081 4141 4201 4261 4321 4381 4441

ATACCGCAAG	TGACCCAGAG	GTGCGGCGAC	CGAAAT
AAGATTCCGA	TCGCCGAAAA	ACAGTCATAA	TAACGICCCG
GAGGGCGTGC	AAAGCGGTCC	GATAAAGAAG	CGTGACATCA
AGGCTTGAGC	CGCTCCAGCG	CGAGTTGCAT	TCACAATTCT
CCAGTGACGA	ATCATCGTCG	ACCTGTCCTA	TTGTGAGCGC
4501 GGTGGCGGGA CCAGTGACGA AGGCTTGAGC GAGGGCGTGC AAGATTCCGA ATACCGCAAG	4561 CGACAGGCCG ATCATCGTCG CGCTCCAGCG AAAGCGGTCC TCGCCGAAAA TGACCCAGAG	CGCTGCCGGC ACCTGTCCTA CGAGTTGCAT GATAAAGAAG ACAGTCATAA GTGCGGCGAC	GACCGGTGAA TTGTGAGCGC TCACAATTCT CGTGACATCA TAACGTCCCG CGAAAT
4501	4561	4621	4681

Figure 52. HLA peptide motif search results

User Parameters and Scoring Information				
method selected to limit number of results	explicit number			
number of results requested	20			
HLA molecule type selected	A_0201			
length selected for subsequences to be scored	9			
echoing mode selected for input sequence	Y			
echoing format	numbered lines			
length of user's input peptide sequence	803			
number of subsequence scores calculated	795			
number of top-scoring subsequences reported back in scoring output table	20			

Scoring Results							
Rank	Start Position	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)				
1	425	MMPKYLNFV	1080.239				
2	410	KLYVRRVFI	642.660				
3	557	RLLKKGYEV	257.342				
4	203	FLVADKVIV	131.175				
5	144	LLHVTDTGV	118.238				
6	547	KEAESSPFV	106.738				
7	639	RLTESPCAL	87.586				
8	381	VTFKSILFV	76.863				
9	3	ALWVLGLCC	41.234				
10	66	VLGLCCVLL	36.316				
11	189	SELIGQFGV	29.023				
12	741	RMLRLSLNI	27.879				
13	451	TÖÖHKTTKA	27.573				
14	280	YVWSSKTET	24.895				
15	259	LELDTIKNL	24.638				
16	417	FITDDFHDM	24.478				
17	467	KTLDMIKKI	17.695				
18	463	KLVRKTLDM	17.388				

19	429	YLNFVKGVV	17.053
20	197	VGFYSAFLV	16.564

Figure 53. Suggested models for transmembrane topology for ICT1025

----> STRONGLY prefered model: N-terminus inside 2 strong transmembrane helices, total score: 2962 # from to length score orientation 1 3 19 (17) 2034 i-o 2 191 212 (22) 928 o-i

-----> alternative model
2 strong transmembrane helices, total score: 2607
from to length score orientation
1 3 19 (17) 1929 o-i
2 191 213 (23) 678 i-o

Figure 54.."DAS" - Transmembrane Prediction server ICT 1025

Start	Stop	Leng	gth∼	Cutoff
6	18	13	~	1.7*
7	17	11	~	2.2
195	209	15	~	1.7*
197	206	10	~	2.2
247	248	2	~	1.7
384	390	7	~	1.7
710	723	14	~	1.7
713	719	7	~	2.2*

Living Cell surface ELISA for screening 1025-antibody containing supernatants in MDA-MB-435 cells

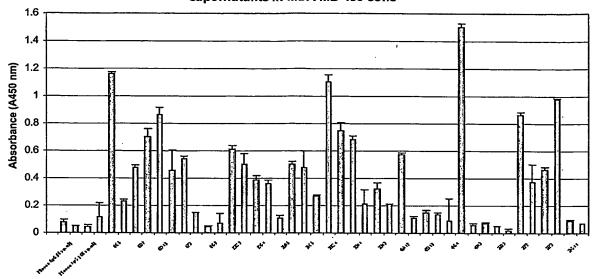


Figure 55. Screening of ICT1025 mAb for surface binding activities in breast tumor cell

The culture supernatants from 40 ICT1025 mAb secreting hybridoma clones were screened for the cell surface binding activities in MDA-MB-435 cells using a live cell surface staining ELISA assay. Mouse IgG at various concentration were used as non-specific controls. The clones with the highest cell surface binding activities (Absorbance value) were selected for mAb purification.

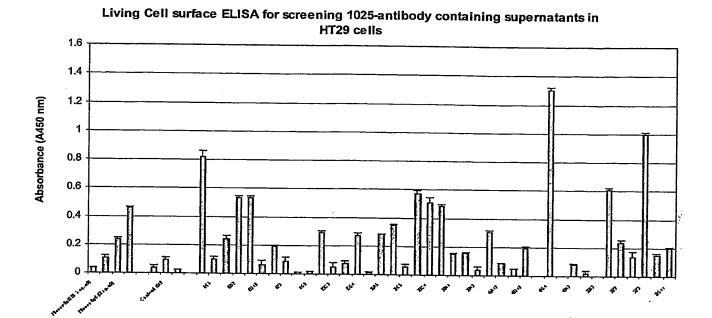
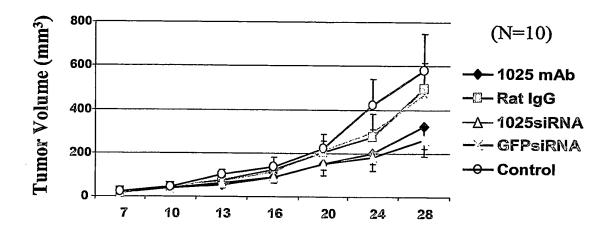


Figure 56. Screening of ICT1025 mAb for surface binding activities in colon tumor cells

The culture supernatants from 40 ICT1025 mAb secreting hybridoma clones were screened for the cell surface binding activities in HT29 cells using a live cell surface staining ELISA assay. Mouse IgG at various concentration were used as non-specific controls. Also, the supernatants from 3 GST mAb secreting hybridoma clones (2H2, 1H2, 3G3) were used as negative controls. The clones with the highest cell surface binding activities (Absorbance value) were selected for mAb purification.



Day Post Tumor Cell Inoculation

Figure 57. Effect of inhibition of 1025 by antibody or siRNA on tumorigenesis and tumor growth. For antibody treatment, 5 million MDA-MB-435 cells were preincubated with 100 ug of 1025 mAb or Rat IgG in a total volume of 1ml culture medium at 37oC for 4 hours. After washing with PBS, the cells were inoculated into the Fat-pat of nude mice at 0.4 million cells per site. For siRNA treatment, 5 million MDA-MB-435 cells in were transfected with 10 ug of 1025 siRNA or GFP siRNA using electroporation, then cells were incubated in a total volume of 1ml culture medium at 37oC for 4 hours. After washing with PBS, the cells were inoculated into the Fat-pat of nude mice at 0.4 million cells per site. For control group, 5 million MDA-MB-435 cells were incubated in a total volume of 1ml culture medium at 37oC for 4 hours. After washing with PBS, the cells were inoculated into the Fat-pat of nude mice at 0.4 million cells per site.